Supplementary Material

| Q-clique 1 | Function Annotation |
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| YLR244C | [F] MAP1 methionine aminopeptidase, isoform 1 |
| YBR283C | [F] SSH1 involved in co-translational pathway of protein transport |
| YBL091C | [F] MAP2 methionine aminopeptidase, isoform 2 |
| YKL024C | [M] URA6 uridine-monophosphate kinase |
| YDR226W | [M] ADK1 adenylate kinase, cytosolic |
| YER170W | [M] ADK2 adenylate kinase, mitochondrial |
| YLR378C | [O] SEC61 ER protein-translocation complex subunit |
| YDR117C | [O] YDR117c similarity to mouse ligatin, a trafficking receptor for phosphoglycoproteins |
| YEL054C | [P] RPL12A 60S large subunit ribosomal protein L12.e |
| YGL135W | [P] RPL1B 60S large subunit ribosomal protein |
| YDL202W | [P] MRPL11 ribosomal protein of the large subunit, mitochondrial |
| YJL177W | [P] RPL17B 60s large subunit ribosomal protein L17.e |
| YDR041W | [P] RSM10 component of the mitochondrial ribosomal small subunit |
| YPR166C | [P] MRP2 ribosomal protein S14 |
| YOR063W | [P] RPL3 60S large subunit ribosomal protein L3.e |
| YPL131W | [P] RPL5 60S large subunit ribosomal protein L5.e |
| YPR102C | [P] RPL11A ribosomal protein L11.e |
| YOL040C | [P] RPS15 40S small subunit ribosomal protein |
| YLR367W | [P] RPS22B ribosomal protein S15a.e.c12 |
| YOL127W | [P] RPL25 ribosomal protein L23a.e |
| YGL147C | [P] RPL9A ribosomal protein L9.e |
| YGL103W | [P] RPL28 60S large subunit ribosomal protein L27a.e |
| YDL136W | [P] RPL35B 60S large subunit ribosomal protein |
| YDL061C | [P] RPS29B ribosomal protein S29.e.B |
| YHR147C | [P] MRPL6 ribosomal protein of the large subunit, mitochondrial |
| YDL191W | [P] RPL35A 60S large subunit ribosomal protein |
| YIL133C | [P] RPL16A 60S large subunit ribosomal protein |
| YNL067W | [P] RPL9B ribosomal protein L9.e.c14 |
| YDR237W | [P] MRPL7 ribosomal protein of the large subunit, mitochondrial |
| YJR145C | [P] RPS4A ribosomal protein S4.e.c10 |
| YBL027W | [P] RPL19B 60S large subunit ribosomal protein L19.e |
| YDL083C | [P] RPS16B ribosomal protein S16.e |
| YEL050C | [P] RML2 ribosomal L2 protein, mitochondrial |
| YMR143W | [P] RPS16A ribosomal protein S16.e |
| YBR251W | [P] MRPS5 ribosomal protein S5, mitochondrial |
| YNL069C | [P] RPL16B 60S large subunit ribosomal protein |
| YBL038W | [P] MRPL16 ribosomal protein of the large subunit, mitochondrial |
| YLR388W | [P] RPS29A ribosomal protein S29.e.A |
| YKL170W | [P] MRPL38 ribosomal protein of the large subunit (L14), mitochondrial |
| YBR146W | [P] MRPS9 ribosomal protein S9 precursor, mitochondrial |
| YNL185C | [P] MRPL19 ribosomal protein of the large subunit, mitochondrial |
| YCR031C | [P] RPS14A 40S Ribosomal protein S14.e |
| YBR048W | [P] RPS11B ribosomal protein S11.e.B |
| YDR012W | [P] RPL4B ribosomal protein L4.e.B |
| YIL018W | [P] RPL2B 60S large subunit ribosomal protein L8.e |
| YJL191W | [P] RPS14B 40S small subunit ribosomal protein S14.e.B |
| YML025C | [P] YML6 ribosomal protein, mitochondrial |
| YBL092W | [P] RPL32 60S large subunit ribosomal protein L32.e |
| YJR123W | [P] RPS5 ribosomal protein S5.e |
| VA (DOCOC) | |
| YMR260C | [P] TIF11 translation initiation factor eIF1a |
| YNR036C | [P] YNR036c strong similarity to ribosomal protein S12 |
| | |
| YNR036C | [P] YNR036c strong similarity to ribosomal protein S12 |

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|--------------------|---|
| YGR085C | [P] RPL11B ribosomal protein |
| YGR034W | [P] RPL26B 60S large subunit ribosomal protein |
| YNL244C | [P] SUI1 translation initiation factor 3 (eIF3) |
| YNL178W | [P] RPS3 ribosomal protein S3.e |
| YGR118W | [P] RPS23A 40S small subunit ribosomal protein S23.e |
| YJL063C | [P] MRPL8 ribosomal protein L17, mitochondrial |
| YGR220C | [P] MRPL9 ribosomal protein YmL9, mitochondrial |
| YMR188C | [P] YMR188c weak similarity to bacterial ribosomal protein S17 |
| YDR025W | [P] RPS11A ribosomal protein S11.e |
| YJL190C | [P] RPS22A ribosomal protein S15a.e.c10 |
| YNL284C | [P] MRPL10 ribosomal protein of the large subunit, mitochondrial |
| YHR203C | [P] RPS4B ribosomal protein S4.e.c8 |
| YML026C | [P] RPS18B ribosomal protein S18.e.c13 |
| YNL306W | [P] MRPS18 ribosomal protein of the small subunit, mitochondrial |
| YGL068W | [P] YGL068w strong similarity to Cricetus mitochrondial ribosomal L12 protein |
| YPL220W | [P] RPL1A ribosomal protein |
| YPR132W | [P] RPS23B 40S small subunit ribosomal protein S23.e |
| YPL183W-A | [P] YPL183w-a strong similarity to mitochondrial and bacterial ribosomal L36 proteins |
| YER117W | [P] RPL23B ribosomal protein L23.e |
| YDR450W | [P] RPS18A ribosomal protein S18.e.c4 |
| YNR037C | [P] RSM19 strong similarity to Mycoplasma ribosomal protein S19 |
| YBR031W | [P] RPL4A ribosomal protein |
| YDR418W | [P] RPL12B 60S large subunit ribosomal protein L12.e |
| YNL081C | [P] YNL081c similarity to ribosomal protein S13 |
| YGL123W | [P] RPS2 40S small subunit ribosomal protein |
| YHL015W | [P] RPS20 ribosomal protein |
| YBL087C | [P] RPL23A 60S large subunit ribosomal protein L23.e |
| YLR340W | [P] RPP0 acidic ribosomal protein L10.e |
| YKL180W | [P] RPL17A ribosomal protein L17.e |
| YLR075W | [P] RPL10 60S large subunit ribosomal protein |
| YLR344W | [P] RPL26A 60S large subunit ribosomal protein |
| YML009C | [P] MRPL39 60S ribosomal protein, mitochondrial |
| YOR150W | [P] MRPL23 ribosomal protein of the large subunit, mitochondrial |
| YBR084C-A | [P] RPL19A 60S large subunit ribosomal protein L19.e |
| YNL292W | [T] PUS4 pseudouridine synthase |
| YPR010C | [T] RPA135 DNA-directed RNA polymerase I, 135 KD subunit |
| YOR116C | [T] RPO31 DNA-directed RNA polymerase III, 160 KD subunit |
| YOR207C YPL212C | [T] RET1 DNA-directed RNA polymerase III, 130 KD subunit |
| | [T] PUS1 pseudouridine synthase 1 [T] RPB3 DNA-directed RNA-polymerase II, 45 kDa |
| YIL021W YGL063W | [T] PUS2 pseudouridine synthase 2 |
| YPR110C | [T] RPC40 DNA-directed RNA polymerase I, III 40 KD subunit |
| YFL001W | [T] DEG1 pseudouridine synthase |
| YBR257W | [T] POP4 involved in processing of tRNAs and rRNAs |
| YLR175W | [T] CBF5 putative rRNA pseuduridine synthase |
| YML010W | [T] SPT5 transcription elongation protein |
| YOR151C | [T] RPB2 DNA-directed RNA polymerase II, 140 kDa chain |
| YOR341W | [T] RPA190 DNA-directed RNA polymerase I, 140 KD alpha subunit |
| YKL009W | [T] MRT4 mRNA turnover 4 |
| YDL140C | [T] RPO21 DNA-directed RNA polymerase II, 215 KD subunit |
| YNL177C | [U] YNL177c similarity to hypothetical protein S. pombe |
| YMR310C | [U] YMR310c similarity to YGR283c |
| YJR014W | [U] YJR014w strong similarity to S.pombe hypothetical protein SPBC16C6.05 |
| YMR158W | [U] YMR158w weak similarity to E.coli ribosomal S8 protein |
| YGR283C | [U] YGR283c similarity to hypothetical protein YMR310c |
| 1 0112030 | 101 1012000 minimity to hypothetical protein 1 mito 100 |

| TIDD 101 G | TYPE TO THE TOTAL THE TOTA |
|------------|--|
| YDR101C | [U] YDR101c weak similarity to proliferation-associated protein |
| Q-clique 2 | Function Annotation |
| YLR244C | [F] MAP1 methionine aminopeptidase, isoform 1 |
| YBR283C | [F] SSH1 involved in co-translational pathway of protein transport |
| YBL091C | [F] MAP2 methionine aminopeptidase, isoform 2 |
| YER170W | [M] ADK2 adenylate kinase, mitochondrial |
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| YKL024C | [M] URA6 uridine-monophosphate kinase |
| YDR117C | [O] YDR117c similarity to mouse ligatin, a trafficking receptor for phosphoglycoproteins |
| YLR378C | [O] SEC61 ER protein-translocation complex subunit |
| YEL054C | [P] RPL12A 60S large subunit ribosomal protein L12.e |
| YGL135W | [P] RPL1B 60S large subunit ribosomal protein |
| YDL202W | [P] MRPL11 ribosomal protein of the large subunit, mitochondrial |
| YDR041W | [P] RSM10 component of the mitochondrial ribosomal small subunit |
| YJL177W | [P] RPL17B 60s large subunit ribosomal protein L17.e |
| YDL136W | [P] RPL35B 60S large subunit ribosomal protein |
| YNL067W | [P] RPL9B ribosomal protein L9.e.c14 |
| YPR102C | [P] RPL11A ribosomal protein L11.e |
| YOL040C | [P] RPS15 40S small subunit ribosomal protein |
| YOL127W | [P] RPL25 ribosomal protein L23a.e |
| YLR367W | [P] RPS22B ribosomal protein S15a.e.c12 |
| YGL147C | [P] RPL9A ribosomal protein L9.e |
| YGL103W | [P] RPL28 60S large subunit ribosomal protein L27a.e |
| YIL133C | [P] RPL16A 60S large subunit ribosomal protein |
| YHR147C | [P] MRPL6 ribosomal protein of the large subunit, mitochondrial |
| YDL061C | [P] RPS29B ribosomal protein S29.e.B |
| YDL191W | [P] RPL35A 60S large subunit ribosomal protein |
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| YLR388W | [P] RPS29A ribosomal protein S29.e.A |
| YKL170W | [P] MRPL38 ribosomal protein of the large subunit (L14), mitochondrial |
| YJR145C | [P] RPS4A ribosomal protein S4.e.c10 |
| YBL027W | [P] RPL19B 60S large subunit ribosomal protein L19.e |
| YDL083C | [P] RPS16B ribosomal protein S16.e |
| YDR012W | [P] RPL4B ribosomal protein L4.e.B |
| YMR143W | [P] RPS16A ribosomal protein S16.e |
| YBR251W | [P] MRPS5 ribosomal protein S5, mitochondrial |
| YNL069C | [P] RPL16B 60S large subunit ribosomal protein |
| YBL038W | [P] MRPL16 ribosomal protein of the large subunit, mitochondrial |
| YBR146W | [P] MRPS9 ribosomal protein S9 precursor, mitochondrial |
| YJL191W | [P] RPS14B 40S small subunit ribosomal protein S14.e.B |
| YNL185C | [P] MRPL19 ribosomal protein of the large subunit, mitochondrial |
| YCR031C | [P] RPS14A 40S Ribosomal protein S14.e |
| YBR048W | [P] RPS11B ribosomal protein S11.e.B |
| YIL018W | [P] RPL2B 60S large subunit ribosomal protein L8.e |
| YML025C | [P] YML6 ribosomal protein, mitochondrial |
| YBL092W | [P] RPL32 60S large subunit ribosomal protein L32.e |
| YJR123W | [P] RPS5 ribosomal protein S5.e |
| YJR113C | [P] RSM7 similarity to bacterial, chloroplast and mitochondrial ribosomal protein S7 |
| YNR036C | [P] YNR036c strong similarity to ribosomal protein S12 |
| YGR085C | [P] RPL11B ribosomal protein |
| YGR034W | [P] RPL26B 60S large subunit ribosomal protein |
| YNL244C | [P] SUI1 translation initiation factor 3 (eIF3) |
| YNL178W | [P] RPS3 ribosomal protein S3.e |
| YGR118W | [P] RPS23A 40S small subunit ribosomal protein S23.e |
| YGR220C | [P] MRPL9 ribosomal protein YmL9, mitochondrial |
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|-------------|---|
| YMR188C | [P] YMR188c weak similarity to bacterial ribosomal protein S17 |
| YDR025W | [P] RPS11A ribosomal protein S11.e |
| YJL190C | [P] RPS22A ribosomal protein S15a.e.c10 |
| YNL284C | [P] MRPL10 ribosomal protein of the large subunit, mitochondrial |
| YHR203C | [P] RPS4B ribosomal protein S4.e.c8 |
| YML026C | [P] RPS18B ribosomal protein S18.e.c13 |
| YNL306W | [P] MRPS18 ribosomal protein of the small subunit, mitochondrial |
| YPL220W | [P] RPL1A ribosomal protein |
| YPR132W | [P] RPS23B 40S small subunit ribosomal protein S23.e |
| YER117W | [P] RPL23B ribosomal protein L23.e |
| YNR037C | [P] RSM19 strong similarity to Mycoplasma ribosomal protein S19 |
| YBR031W | [P] RPL4A ribosomal protein |
| YDR450W | [P] RPS18A ribosomal protein S18.e.c4 |
| YNL081C | [P] YNL081c similarity to ribosomal protein S13 |
| YGL123W | [P] RPS2 40S small subunit ribosomal protein |
| YDR418W | [P] RPL12B 60S large subunit ribosomal protein L12.e |
| YHL015W | [P] RPS20 ribosomal protein |
| YBL087C | [P] RPL23A 60S large subunit ribosomal protein L23.e |
| YKL180W | [P] RPL17A ribosomal protein L17.e |
| YLR340W | [P] RPP0 acidic ribosomal protein L10.e |
| YLR075W | [P] RPL10 60S large subunit ribosomal protein |
| YLR344W | [P] RPL26A 60S large subunit ribosomal protein |
| YPR166C | [P] MRP2 ribosomal protein S14 |
| YOR150W | [P] MRPL23 ribosomal protein of the large subunit, mitochondrial |
| YBR084C-A | [P] RPL19A 60S large subunit ribosomal protein L19.e |
| YOR063W | [P] RPL3 60S large subunit ribosomal protein L3.e |
| YBR257W | [T] POP4 involved in processing of tRNAs and rRNAs |
| YOR341W | [T] RPA190 DNA-directed RNA polymerase I, 190 KD alpha subunit |
| YOR116C | [T] RPO31 DNA-directed RNA polymerase III, 160 KD subunit |
| YOR207C | [T] RET1 DNA-directed RNA polymerase III, 130 KD subunit |
| YPL212C | [T] PUS1 pseudouridine synthase 1 |
| YIL021W | [T] RPB3 DNA-directed RNA-polymerase II, 45 kDa |
| YGL063W | [T] PUS2 pseudouridine synthase 2 |
| YFL001W | [T] DEG1 pseudouridine synthase |
| YPR110C | [T] RPC40 DNA-directed RNA polymerase I, III 40 KD subunit |
| YOR151C | [T] RPB2 DNA-directed RNA polymerase II, 140 kDa chain |
| YML010W | [T] SPT5 transcription elongation protein |
| YDL140C | [T] RPO21 DNA-directed RNA polymerase II, 215 KD subunit |
| YNL292W | [T] PUS4 pseudouridine synthase |
| YNL177C | [U] YNL177c similarity to hypothetical protein S. pombe |
| YMR310C | [U] YMR310c similarity to YGR283c |
| YJR014W | [U] YJR014w strong similarity to S.pombe hypothetical protein SPBC16C6.05 |
| YGR283C | [U] YGR283c similarity to hypothetical protein YMR310c |
| YMR158W | [U] YMR158w weak similarity to E.coli ribosomal S8 protein |
| Q-clique 3 | Function Annotation |
| YNL132W | [C] KRE33 similarity to A.ambisexualis antheridiol steroid receptor |
| YCR057C | [C] PWP2 periodic tryptophan protein |
| YMR128W | [C] ECM16 putative DEAH-box RNA helicase |
| YGR245C | [D] SDA1 required for normal organization of the actin cytoskeleton; required for passage |
| | through Start |
| YMR290C | [D] HAS1 helicase associated with SET1P |
| YLR129W | |
| | [D] DIP2 DOM34P-interacting protein |
| YPL126W | [D] NAN1 weak similarity to fruit fly TFIID subunit p85 |
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| YLR002C | [F] NOC3 required for maturation and intranuclear transport of pre-ribosomes |
| YBR247C | [F] ENP1 effects N-glycosylation |
| YDR299W | [O] BFR2 involved in protein transport steps at the Brefeldin A blocks |
| YOR206W | [O] NOC2 crucial for intranuclear movement of ribosomal precursor particles |
| YER006W | [O] YER006w similarity to P.polycephalum myosin-related protein mlpA |
| YDR060W | [P] MAK21 protein required for 60S ribosomal subunit biogenesis |
| YDL148C | [P] NOP14 nuclear and nucleolar protein with possible role in ribosome biogenesis |
| YCL054W | [P] SPB1 required for ribosome synthesis, putative methylase |
| YPR016C | [P] TIF6 translation initiation factor 6 (eIF6) |
| YLR197W | [T] SIK1 involved in pre-rRNA processing |
| YDL031W | [T] DBP10 putative RNA helicase involved in ribosome biogenesis |
| YKL172W | [T] EBP2 required for pre-rRNA processing and ribosomal subunit assembly |
| YPL217C | [T] BMS1 GTP-binding protein, required for distinct steps of 40S ribosome biogenesis |
| YDR087C | [T] RRP1 involved in processing rRNA precursor species to mature rRNAs |
| YHR148W | [T] IMP3 component of the U3 small nucleolar ribonucleoprotein |
| YPL211W | [T] NIP7 required for efficient 60S ribosome subunit biogenesis |
| YLL011W | [T] SOF1 involved in 18S pre-rRNA production |
| YPL043W | [T] NOP4 nucleolar protein |
| YLL008W | [T] DRS1 RNA helicase of the DEAD box family |
| YJR002W | [T] MPP10 component of the U3 small nucleolar ribonucleoprotein |
| YGL019W | [T] CKB1 casein kinase II, beta subunit |
| YDL014W | [T] NOP1 fibrillarin |
| YNL061W | [T] NOP2 nucleolar protein |
| YFL002C | [T] SPB4 ATP-dependent RNA helicase of DEAH box family |
| YKL009W | [T] MRT4 mRNA turnover 4 |
| YGR145W | [U] YGR145w similarity to C.elegans hypothetical protein |
| YLR222C | [U] CST29 similarity to DIP2P |
| YER082C | [U] KRE31 similarity to M.sexta steroid regulated MNG10 protein |
| YGR090W | [U] YGR090w similarity to PIR:T40678 hypothetical protein SPBC776.08c S. pombe |
| YGR128C | [U] YGR128c hypothetical protein |
| YDR449C | [U] YDR449c similarity to hypothetical protein S. pombe |
| YNR053C | [U] NOG2 strong similarity to human breast tumor associated autoantigen |
| YMR049C | [U] ERB1 weak similarity to A.thaliana PRL1 protein |
| YHR088W | [U] RPF1 similarity to hypothetical protein YNL075w |
| YDR496C | [U] PUF6 similarity to hypothetical human and C.elegans proteins |
| YGL111W | [U] YGL111w weak similarity to hypothetical protein S. pombe |
| YLR186W | [U] EMG1 strong similarity to S.pombe hypothetical protein C18G6.07C |
| YMR093W | [U] YMR093w weak similarity to PWP2P |
| YNL182C | [U] YNL182c weak similarity to S.pombe hypothetical protein |
| YOL077C | [U] BRX1 strong similarity to C.elegans K12H4.3 protein |
| YDR101C | [U] YDR101c weak similarity to proliferation-associated protein |
| YKL014C | [U] YKL014c similarity to hypothetical protein SPCC14G10.02 S. pombe |
| YPL012W | [U] RRP12 hypothetical protein |
| YDR324C | [U] YDR324c weak similarity to beta transducin from S. pombe and other WD-40 repeat |
| | containing proteins |
| YPR144C | [U] YPR144c similarity to YDR060w and C.elegans hypothetical protein |
| YPL093W | [U] NOG1 similarity to M.jannaschii GTP-binding protein |
| YNL002C | [U] RLP7 strong similarity to mammalian ribosomal L7 proteins |
| YHR052W | [U] CIC1 adaptor protein specifically linking the 26S proteasome to its substrate, the SCF |
| | component CDC4 |
| YOL041C | [U] NOP12 weak similarity to M.sativa NUM1, hnRNP protein from C. tentans and D. |
| | melanogaster, murine/bovine poly(A) binding protein II, and NSR1P |
| YKR060W | [U] YKR060w similarity to hypothetical protein S. pombe |
| YGR103W | [U] RRP13 similarity to zebrafish essential for embryonic development gene pescadillo |
| YBL004W | [U] YBL004w weak similarity to Papaya ringspot virus polyprotein |

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| HR197W [U] YHR197w weak similarity to PIR:T22172 hypothetical protein F44E5.2 C. elegans | 3 |
| LR409C [U] YLR409c strong similarity to S. pombe beta-transducin | |
| LR276C [U] DBP9 similarity to YDL031w, MAK5P and RNA helicases | |
| KR081C [U] YKR081c strong similarity to hypothetical protein S. pombe | |
| ER126C [U] KRE32 weak similarity to E.coli colicin N | |
| [U] YJL109c weak similarity to ATPase DRS2P | |
| NL110C [U] YNL110c weak similarity to fruit fly RNA-binding protein | |
| clique 4 Function Annotation | |
| HR066W [C] SSF1 mating protein | |
| GR245C [D] SDA1 required for normal organization of the actin cytoskeleton; required for pathrough Start | ssage |
| MR290C [D] HAS1 helicase associated with SET1P | |
| OR272W [D] YTM1 microtubule-interacting protein | |
| LR449W [F] FPR4 nucleolar peptidylprolyl cis-trans isomerase (PPIase) | |
| LR002C [F] NOC3 required for maturation and intranuclear transport of pre-ribosomes | |
| OR206W [O] NOC2 crucial for intranuclear movement of ribosomal precursor particles | |
| ER006W [O] YER006w similarity to P.polycephalum myosin-related protein mlpA | |
| PR016C [P] TIF6 translation initiation factor 6 (eIF6) | |
| DR060W [P] MAK21 protein required for 60S ribosomal subunit biogenesis | |
| CL054W [P] SPB1 required for ribosome synthesis, putative methylase | |
| NL061W [T] NOP2 nucleolar protein | |
| KL172W [T] EBP2 required for pre-rRNA processing and ribosomal subunit assembly | |
| PL043W [T] NOP4 nucleolar protein | |
| DL031W [T] DBP10 putative RNA helicase involved in ribosome biogenesis | |
| FL002C [T] SPB4 ATP-dependent RNA helicase of DEAH box family | |
| KL009W [T] MRT4 mRNA turnover 4 | |
| LL008W [T] DRS1 RNA helicase of the DEAD box family | |
| DR087C [T] RRP1 involved in processing rRNA precursor species to mature rRNAs | |
| DL051W [T] LHP1 RNA binding protein | |
| PL211W [T] NIP7 required for efficient 60S ribosome subunit biogenesis | |
| BR142W [T] MAK5 ATP-dependent RNA helicase | |
| NL182C [U] YNL182c weak similarity to S.pombe hypothetical protein | |
| LR106C [U] YLR106c similarity to Kaposi's sarcoma-associated herpes-like virus ORF73 hor | nolog |
| gene | _ |
| FR001W [U] LOC1 weak similarity to rabbit triadin SPP41P | |
| KR081C [U] YKR081c strong similarity to hypothetical protein S. pombe | |
| NL110C [U] YNL110c weak similarity to fruit fly RNA-binding protein | |
| DR496C [U] PUF6 similarity to hypothetical human and C.elegans proteins | |
| DR101C [U] YDR101c weak similarity to proliferation-associated protein | |
| OL077C [U] BRX1 strong similarity to C.elegans K12H4.3 protein | |
| HR197W [U] YHR197w weak similarity to PIR:T22172 hypothetical protein F44E5.2 C. elegans | 3 |
| KL014C [U] YKL014c similarity to hypothetical protein SPCC14G10.02 S. pombe | |
| GR103W [U] RRP13 similarity to zebrafish essential for embryonic development gene pescadillo |) |
| GL111W [U] YGL111w weak similarity to hypothetical protein S. pombe | |
| PL093W [U] NOG1 similarity to M.jannaschii GTP-binding protein | |
| OL041C [U] NOP12 weak similarity to M.sativa NUM1, hnRNP protein from C. tentans ar | nd D. |
| melanogaster, murine/bovine poly(A) binding protein II, and NSR1P | |
| HR052W [U] CIC1 adaptor protein specifically linking the 26S proteasome to its substrate, the | SCF |
| component CDC4 | |
| NL002C [U] RLP7 strong similarity to mammalian ribosomal L7 proteins | |
| HR088W [U] RPF1 similarity to hypothetical protein YNL075w | |
| 1K088W [O] KFT1 similarity to hypothetical protein 1NL073W | |
| MR049C [U] ERB1 weak similarity to A.thaliana PRL1 protein | |
| | |
| MR049C [U] ERB1 weak similarity to A.thaliana PRL1 protein | |

| VED 12CC | IIII VDE22 |
|--------------------|--|
| YER126C | [U] KRE32 weak similarity to E.coli colicin N |
| Q-clique 5 | Function Annotation |
| YNL132W | [C] KRE33 similarity to A.ambisexualis antheridiol steroid receptor |
| YMR128W | [C] ECM16 putative DEAH-box RNA helicase |
| YCR057C | [C] PWP2 periodic tryptophan protein |
| YLR129W | [D] DIP2 DOM34P-interacting protein |
| YPL126W | [D] NAN1 weak similarity to fruit fly TFIID subunit p85 |
| YBR247C | [F] ENP1 effects N-glycosylation |
| YDR299W | [O] BFR2 involved in protein transport steps at the Brefeldin A blocks |
| YDL148C | [P] NOP14 nuclear and nucleolar protein with possible role in ribosome biogenesis [T] BMS1 GTP-binding protein, required for distinct steps of 40S ribosome biogenesis |
| YPL217C YDL014W | [T] NOP1 fibrillarin |
| | |
| YLL011W YOR061W | [T] SOF1 involved in 18S pre-rRNA production [T] CKA2 casein kinase II alpha' chain |
| YLR197W | [T] SIK1 involved in pre-rRNA processing |
| YER127W | [T] LCP5 NGG1P interacting protein |
| YIL035C | [T] CKA1 casein kinase II, catalytic alpha chain |
| YHR148W | [T] IMP3 component of the U3 small nucleolar ribonucleoprotein |
| YOR039W | [T] CKB2 casein kinase II beta' chain |
| YJR002W | [T] MPP10 component of the U3 small nucleolar ribonucleoprotein |
| YGL019W | [T] CKB1 casein kinase II, beta subunit |
| YPR144C | [U] YPR144c similarity to YDR060w and C.elegans hypothetical protein |
| YGR145W | [U] YGR145w similarity to C.elegans hypothetical protein |
| YLR222C | [U] CST29 similarity to DIP2P |
| YGR090W | [U] YGR090w similarity to PIR:T40678 hypothetical protein SPBC776.08c S. pombe |
| YER082C | [U] KRE31 similarity to M.sexta steroid regulated MNG10 protein |
| YLR186W | [U] EMG1 strong similarity to S.pombe hypothetical protein C18G6.07C |
| YKR060W | [U] YKR060w similarity to hypothetical protein S. pombe |
| YJL069C | [U] YJL069c similarity to C.elegans hypothetical protein |
| YBL004W | [U] YBL004w weak similarity to Papaya ringspot virus polyprotein |
| YLR409C | [U] YLR409c strong similarity to S. pombe beta-transducin |
| YGR128C | [U] YGR128c hypothetical protein |
| YMR093W | [U] YMR093w weak similarity to PWP2P |
| YDR449C | [U] YDR449c similarity to hypothetical protein S. pombe |
| YKL099C | [U] YKL099c similarity to C.elegans hypothetical proteins C18G6.06 and C16C10.2 |
| YHR196W | [U] YHR196w weak similarity to YDR398w |
| YJL109C | [U] YJL109c weak similarity to ATPase DRS2P |
| YDR324C | [U] YDR324c weak similarity to beta transducin from S. pombe and other WD-40 repeat |
| | containing proteins |
| YOR145C | [U] YOR145c strong similarity to hypothetical S. pombe protein and to hypothetical C. |
| | elegans protein |
| Q-clique 6 | Function Annotation |
| YDR117C | [O] YDR117c similarity to mouse ligatin, a trafficking receptor for phosphoglycoproteins |
| YJL177W | [P] RPL17B 60s large subunit ribosomal protein L17.e |
| YDR025W | [P] RPS11A ribosomal protein S11.e |
| YNL244C | [P] SUI1 translation initiation factor 3 (eIF3) |
| YJL190C | [P] RPS22A ribosomal protein S15a.e.c10 |
| YDR012W | [P] RPL4B ribosomal protein L4.e.B |
| YHR203C | [P] RPS4B ribosomal protein S4.e.c8 |
| YER117W | [P] RPL23B ribosomal protein L23.e |
| YPR102C | [P] RPL11A ribosomal protein L11.e |
| YLR367W | [P] RPS22B ribosomal protein S15a.e.c12 |
| YGL147C | [P] RPL9A ribosomal protein L9.e |
| YBR031W | [P] RPL4A ribosomal protein |
| YDL061C | [P] RPS29B ribosomal protein S29.e.B |

| Q-clique 8 | Function Annotation |
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| | 1 J The Trans Paranet |
| YBR253W | [T] SRB6 DNA-directed RNA polymerase II suppressor protein |
| YBR193C | [T] MED8 transcriptional regulation mediator |
| | subcomplex subunit |
| YGR104C | [T] SRB5 DNA-directed RNA polymerase II holoenzyme and Kornberg's mediator (SRB) |
| YOR174W | [T] MED4 transcription regulation mediator |
| YNR010W | [T] CSE2 subunit of RNA polymerase II mediator complex |
| 1213000 | subcomplex subunit |
| YDR308C | [T] SRB7 DNA-directed RNA polymerase II holoenzyme and kornberg's mediator (SRB) |
| 10103170 | subcomplex subunit |
| YOL051W | [T] GAL11 DNA-directed RNA polymerase II holoenzyme and Kornberg's mediator (SRB) |
| 1 CIXUO1 W | subunit |
| YCR081W | [T] SRB8 DNA-directed RNA polymerase II holoenzyme and Srb10 CDK subcomplex |
| YPR070W | [T] MED1 component of RNA polymerase II holoenzyme and mediator subcomplex |
| YLR071C | [T] RGR1 DNA-directed RNA polymerase II holoenzyme subunit |
| 11110410 | subcomplex subunit |
| YHR041C | [T] SRB2 DNA-directed RNA polymerase II holoenzyme and Kornberg's mediator (SRB) |
| 1 L1XU22 VV | subcomplex subunit |
| YER022W | [T] SRB4 DNA-directed RNA polymerase II holoenzyme and Kornberg's mediator (SRB) |
| 1004430 | subunit |
| YDR443C | [T] SSN2 DNA-directed RNA polymerase II holoenzyme and Srb10 CDK subcomplex |
| YMR112C | [T] MED11 mediator complex subunit |
| YPL042C | [D] SSN3 cyclin-dependent CTD kinase |
| YGL127C | [B] SOH1 allows HPR1 null mutant to grow at 37 deg. |
| YML007W | [B] YAP1 transcriptional activator involved in oxidative stress response |
| YNL236W | [B] SIN4 global regulator protein |
| YOL148C | [B] SPT20 member of the TBP class of SPT proteins that alter transcription site selection |
| YGL025C | [B] PGD1 mediator complex subunit |
| YPR168W | [B] NUT2 negative transcription regulator from artifical reporters |
| YOL135C | [B] MED7 member of RNA Polymerase II transcriptional regulation mediator complex |
| YHR058C | [B] MED6 RNA polymerase II transcriptional regulation mediator |
| YGL151W | [B] NUT1 negative transcription regulator from artifical reporters |
| Q-clique 7 | Function Annotation |
| YGR283C | [U] YGR283c similarity to hypothetical protein YMR310c |
| YMR158W | [U] YMR158w weak similarity to E.coli ribosomal S8 protein |
| YJR014W | [U] YJR014w strong similarity to S.pombe hypothetical protein SPBC16C6.05 |
| YMR310C | [U] YMR310c similarity to YGR283c |
| YNL177C | [U] YNL177c similarity to hypothetical protein S. pombe |
| YBR257W | [T] POP4 involved in processing of tRNAs and rRNAs |
| YKL170W | [P] MRPL38 ribosomal protein of the large subunit (L14), mitochondrial |
| YLR388W | [P] RPS29A ribosomal protein S29.e.A |
| YGR085C | [P] RPL11B ribosomal protein |
| YDR237W | [P] MRPL7 ribosomal protein of the large subunit, mitochondrial |
| YNL067W | [P] RPL9B ribosomal protein L9.e.c14 |
| YPR166C | [P] MRP2 ribosomal protein S14 |
| YBR084C-A | [P] RPL19A 60S large subunit ribosomal protein L19.e |
| YBL092W | [P] RPL32 60S large subunit ribosomal protein L32.e |
| YML025C | [P] YML6 ribosomal protein, mitochondrial |
| YBR048W | [P] RPS11B ribosomal protein S11.e.B |
| YJR145C | [P] RPS4A ribosomal protein S4.e.c10 |
| YBL027W | [P] RPL19B 60S large subunit ribosomal protein L19.e |
| YKL180W | [P] RPL17A ribosomal protein L17.e |
| YBL087C | [P] RPL23A 60S large subunit ribosomal protein L23.e |
| YHR147C | [P] MRPL6 ribosomal protein of the large subunit, mitochondrial |

| VIDS-64C. [D] CDL-40 cell division control protein VML049C [O] RSB1 involved in RNA splicing and ER to Golgi transport VKL173W [P] SNU114 US snRNP-specific protein VGL128C [R] VGL128C weak similarity to dnal proteins VLR298C [T] YHC1 associated with the U1 snRNP complex VGR074W [T] SMD1 snRNA-associated protein VTL0.36C [T] PRP19 non-snRNP sliccosome component required for DNA repair VPL178W [T] CBC2 small subunit of the nuclear cap-binding protein complex CBC VTJL203W [T] PRP21 pre-mRNA splicing factor VGR013W [T] SNU11 associated with U1 snRNP, no counterpart in mammalian U1 snRNP VPL213W [T] LEA1 U2 A' snRNP protein VTR0416W [T] SNV11 associated with U1 snRNP, no counterpart in mammalian U1 snRNP VPL213W [T] LEA1 U2 A' snRNP protein VTR0416W [T] SYP1 symtetric feltal with CDC40 VTDL043C [T] SNP11 U1 small nuclear ribonucleoprotein VTR240C [T] SNP1 U1 small nuclear ribonucleoprotein VTR240C [T] SNP1 U1 small nuclear ribonucleoprotein VTR288W [T] SND1 slug ssociated with U1 snRNP as part of the Sm-core that is common to all spliceosomal snRNPs VGL120C [T] PRP45 pre-mRNA splicing factor VTR040W [T] FRP41 pre-mRNA splicing factor VTR050W [T] FRP43 involved in spliceosome disassembly VTR120C [T] SNP1 U1 snRNP protein spliceosome disassembly VTR120C [T] FRP45 pre-mRNA splicing factor (snRNA-associated protein) VTR19W [T] FRP40 pre-mRNA splicing factor (snRNA-associated protein) VTR19W [T] FRP30 pre-mRNA splicing protein VTR040W [T] FRP30 pre-mRNA splicing protein VTR19W [T] FRP40 splicing factor VTR19W [T] FRP30 pre-mRNA splicing factor (snRNA-associated protein) VTR240C [T] FRP40 splicing factor VTR15W [T] FRP40 splicing factor VTR240C [T] FRP40 splicing factor VTR413C [T] FRP40 spli | VDD264C | ID1 (DC(40 11 1' ' ' ' ' ' ' ' 1 ' ' ' ' |
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| VKL13W P SNU114 US saRNP-specific protein | YDR364C | [D] CDC40 cell division control protein |
| YGL128C R YGL128c weak similarity to dnal proteins YLR298C T YHC1 associated with the U1 snRNP complex YGR074W T SMD1 snRNA-associated protein YLL036C T PRP19 non-snRNP sliceosome component required for DNA repair YPL178W T GRC2 small subunit of the nuclear cap-binding protein complex CBC YJL203W T PRP21 pre-mRNA splicing factor YBR055C T PRP6 snRNP(U4/U6)-associated splicing factor YGR013W T SND11 associated with U1 snRNP, no counterpart in mammalian U1 snRNP YPL1213W T LEA1 U2 A' snRNP protein YPL1213W T LEA1 U2 A' snRNP protein YPL1213W T NAMR meiotic recombination protein YDR416W T SNF1 synthetic lethal with CDC40 YDL043C T PRP11 pre-mRNA splicing factor YDR240C T SNS05 U1 snRNA protein, no counterpart in mammalian snRNP YIL061C T SNP1 U1 small nuclear ribonucleoprotein YMR288W YAL032C T PRP45 pre-mRNA splicing factor YT SNS05 U1 snRNA protein, no counterpart in mammalian snRNP YIL061C T SNP1 U1 small nuclear ribonucleoprotein YER029C T PRP43 involved in spliceosome disassembly YHR125W T ST01 lange subunit of the nuclear cap-binding protein complex CBC YDL030W T PRP3 involved in spliceosome disassembly YMR125W T ST01 lange subunit of the nuclear cap-binding protein complex CBC YDL030W T PRP9 pre-mRNA splicing factor (snRNA-associated protein) YBR119W T MUD1 U1 snRNP-specific A protein YML046W T PRP30 pre-mRNA splicing factor YPR138W T PRP40 splicing factor YPR138W T PRP40 splicing factor YPR240C T PRP40 splicing factor YDL087C T T SMD2 U1 snRNP protein with a role in 5' splice site recognition YMR240C T SMD3 spliceosomal snRNPs YRR178W T SMD2 U1 snRNP protein of the Sm class YDL030W T PRP40 splicing factor YPR50W T SMD3 splicing factor YPR50W T SMD3 splicing factor YDL087C T SMD3 splicing factor YDL087C T SMD3 splicing factor YDL087C T SMD3 splicing factor YDL087W T SMD3 splicing factor YDL087W T SMD3 splicing facto | | |
| YIROJAW TJ SMD1 sasociated with the U1 saRNP complex | | |
| VCR074W T] SMD1 snRNA-associated protein | | |
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| YPL178W | | |
| Syll-203W Ti PRP2 pre-mRNA splicing factor | | |
| VRR05SC | | 1 01 1 |
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| YDL043C | | |
| YDR.240C | | · |
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| YMR288W [T] HSH155 component of a multiprotein splicing factor YAL032C [T] PRP45 pre-mRNA splicing factor YER029C [T] SMB1 associated with U1 snRNP as part of the Sm-core that is common to all spliceosomal snRNPs YGL120C [T] PRP43 involved in spliceosome disassembly YMR125W [T] STO1 large subunit of the nuclear cap-binding protein complex CBC YDL030W [T] PRP9 pre-mRNA splicing factor (snRNA-associated protein) YBR119W [T] MUD1 U1 snRNP-specific A protein YGR091W [T] PRP31 pre-mRNA splicing factor YML046W [T] PRP39 pre-mRNA splicing factor YML046W [T] PRP39 pre-mRNA splicing factor YPR178W [T] PRP40 splicing factor YPL087C [T] FUC7 yeast U1 snRNP protein with a role in 5' splice site recognition YMR240C [T] CUS1 U2 snRNP protein of the Sm class YOR308C [T] SMD2 U1 snRNP protein of the Sm class YOR308C [T] SMD2 U1 snRNP protein of the Sm class YOR308C [T] SMD2 U1 snRNP associated protein, required for pre-mRNA splicing YPR101W [T] SNT309 splicing factor YGR278W [U] YGR278w similarity to Celegans LET-858 [U] YGR278w similarity to Celegans LET-858 [U] YGR278w similarity to Celegans LET-858 [U] YLR424W [U] YLR424w weak similarity to STU1P Q-clique 9 YEntotion Annotation YMR128W YMR128W [C] ECM16 putative DEAH-box RNA helicase YNL132W [C] KR33 similarity to A.ambisexualis antheridiol steroid receptor YCR057C [C] PWP2 periodic tryptophan protein YPR247C [F] ENP1 effects N-glycosylation YDR299W [D] DNAN1 weak similarity to fruit fly TFIID subunit p85 YLL126W [D] NAN1 weak similarity to fruit fly TFIID subunit p85 YLL126W [D] DNA94-interacting protein transport steps at the Brefeldin A blocks YYLL148C [P] NOP14 nuclear and nucleolar protein with possible role in ribosome biogenesis YHR148W [T] IMP3 component of the U3 small nucleolar ribonucleoprotein YILL011W [T] SOF1 involved in protein transport steps at the Brefeldin A blocks YYLL148C [T] ENP14 interacting protein interacting protein [T] CKA2 casein kinase II alpha' chain YER127W [T] LCP5 NGGIP interacting protein | | |
| Yaliasco (T) PRP45 pre-mRNA splicing factor YER029C (T) SMB1 associated with U1 snRNP as part of the Sm-core that is common to all spliceosomal snRNPs YGL120C (T) PRP43 involved in spliceosome disassembly YMR125W (T) STO1 large subunit of the nuclear cap-binding protein complex CBC YDL030W (T) PRP9 pre-mRNA splicing factor (snRNA-associated protein) YBR119W (T) MUD1 U1 snRNP-specific A protein YGR091W (T) PRP31 pre-mRNA splicing protein YMR1046W (T) PRP31 pre-mRNA splicing factor YPL178W (T) PRP40 splicing factor YPL178W (T) PRP40 splicing factor YYLL0187C (T) LUC7 yeast U1 snRNP protein with a role in 5' splice site recognition YMR240C (T) CUS1 U2 snRNP protein of the Sm class YOR308C (T) SMD2 U1 snRNP protein of the Sm class YOR308C (T) SMD2 U1 snRNP protein of the Sm class YOR308C (T) SND6 component of U4/U6.U5 snRNP YLR147C (T) SMD3 spliceosomal snRNA-associated Sm core protein required for pre-mRNA splicing YPR101W (T) SNT309 splicing factor YGR278W (U) YGR278w similarity to C.elegans LET-858 YDL209C (U) YDL209c similarity to hypothetical S, pombe protein YLR424W (U) YLR424w weak similarity to STU1P Q-clique 9 Function Annotation YMR128W (C) ECM16 putative DEAH-box RNA helicase YNL132W (C) KR33 similarity to A.ambisexualis antheridiol steroid receptor YCR057C (C) PW2 periodic tryptophan protein YBR247C (F) ENP1 effects N-glycosylation YBR247C (F) ENP1 effects N-glycosylation (T) ENP260 (T) MNA1 weak similarity to fruit fly TFIID subunit p85 YLR148W (T) IMP3 component of the U3 small nucleolar ribonucleoprotein YHL184C (T) ENP260 (T) STU1P (T) ENP260 (T) ENP260 (T) STU1P (T) ENP260 | | |
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| YGR278W [U] YGR278w similarity to C.elegans LET-858 YDL209C [U] YDL209c similarity to hypothetical S. pombe protein YPL151C [U] PRP46 strong similarity to A.thaliana PRL1 and PRL2 proteins YLR424W [U] YLR424w weak similarity to STU1P Q-clique 9 Function Annotation YMR128W [C] ECM16 putative DEAH-box RNA helicase YNL132W [C] KRE33 similarity to A.ambisexualis antheridiol steroid receptor YCR057C [C] PWP2 periodic tryptophan protein YPL126W [D] NAN1 weak similarity to fruit fly TFIID subunit p85 YLR129W [D] DIP2 DOM34P-interacting protein YBR247C [F] ENP1 effects N-glycosylation YDR299W [O] BFR2 involved in protein transport steps at the Brefeldin A blocks YDL148C [P] NOP14 nuclear and nucleolar protein with possible role in ribosome biogenesis YHR148W [T] IMP3 component of the U3 small nucleolar ribonucleoprotein YLL011W [T] SOF1 involved in 18S pre-rRNA production YOR061W [T] CKA2 casein kinase II alpha' chain YER127W [T] LCP5 NGG1P interacting protein | | |
| YDL209C [U] YDL209c similarity to hypothetical S. pombe protein YPL151C [U] PRP46 strong similarity to A.thaliana PRL1 and PRL2 proteins YLR424W [U] YLR424w weak similarity to STU1P Q-clique 9 Function Annotation YMR128W [C] ECM16 putative DEAH-box RNA helicase YNL132W [C] KRE33 similarity to A.ambisexualis antheridiol steroid receptor YCR057C [C] PWP2 periodic tryptophan protein YPL126W [D] NAN1 weak similarity to fruit fly TFIID subunit p85 YLR129W [D] DIP2 DOM34P-interacting protein YBR247C [F] ENP1 effects N-glycosylation YDR299W [O] BFR2 involved in protein transport steps at the Brefeldin A blocks YDL148C [P] NOP14 nuclear and nucleolar protein with possible role in ribosome biogenesis YHR148W [T] IMP3 component of the U3 small nucleolar ribonucleoprotein YLL011W [T] SOF1 involved in 18S pre-rRNA production YOR061W [T] CKA2 casein kinase II alpha' chain YER127W [T] LCP5 NGG1P interacting protein | | |
| YPL151C [U] PRP46 strong similarity to A.thaliana PRL1 and PRL2 proteins YLR424W [U] YLR424w weak similarity to STU1P Q-clique 9 Function Annotation YMR128W [C] ECM16 putative DEAH-box RNA helicase YNL132W [C] KRE33 similarity to A.ambisexualis antheridiol steroid receptor YCR057C [C] PWP2 periodic tryptophan protein YPL126W [D] NAN1 weak similarity to fruit fly TFIID subunit p85 YLR129W [D] DIP2 DOM34P-interacting protein YBR247C [F] ENP1 effects N-glycosylation YDR299W [O] BFR2 involved in protein transport steps at the Brefeldin A blocks YDL148C [P] NOP14 nuclear and nucleolar protein with possible role in ribosome biogenesis YHR148W [T] IMP3 component of the U3 small nucleolar ribonucleoprotein YLL011W [T] SOF1 involved in 18S pre-rRNA production YOR061W [T] CKA2 casein kinase II alpha' chain YER127W [T] LCP5 NGG1P interacting protein | | |
| YLR424W [U] YLR424w weak similarity to STU1P Q-clique 9 Function Annotation YMR128W [C] ECM16 putative DEAH-box RNA helicase YNL132W [C] KRE33 similarity to A.ambisexualis antheridiol steroid receptor YCR057C [C] PWP2 periodic tryptophan protein YPL126W [D] NAN1 weak similarity to fruit fly TFIID subunit p85 YLR129W [D] DIP2 DOM34P-interacting protein YBR247C [F] ENP1 effects N-glycosylation YDR299W [O] BFR2 involved in protein transport steps at the Brefeldin A blocks YDL148C [P] NOP14 nuclear and nucleolar protein with possible role in ribosome biogenesis YHR148W [T] IMP3 component of the U3 small nucleolar ribonucleoprotein YLL011W [T] SOF1 involved in 18S pre-rRNA production YOR061W [T] CKA2 casein kinase II alpha' chain YER127W [T] LCP5 NGG1P interacting protein | | , , , , , , , , , , , , , , , , , , , |
| Q-clique 9Function AnnotationYMR128W[C] ECM16 putative DEAH-box RNA helicaseYNL132W[C] KRE33 similarity to A.ambisexualis antheridiol steroid receptorYCR057C[C] PWP2 periodic tryptophan proteinYPL126W[D] NAN1 weak similarity to fruit fly TFIID subunit p85YLR129W[D] DIP2 DOM34P-interacting proteinYBR247C[F] ENP1 effects N-glycosylationYDR299W[O] BFR2 involved in protein transport steps at the Brefeldin A blocksYDL148C[P] NOP14 nuclear and nucleolar protein with possible role in ribosome biogenesisYHR148W[T] IMP3 component of the U3 small nucleolar ribonucleoproteinYLL011W[T] SOF1 involved in 18S pre-rRNA productionYOR061W[T] CKA2 casein kinase II alpha' chainYER127W[T] LCP5 NGG1P interacting protein | | |
| YMR128W [C] ECM16 putative DEAH-box RNA helicase YNL132W [C] KRE33 similarity to A.ambisexualis antheridiol steroid receptor YCR057C [C] PWP2 periodic tryptophan protein YPL126W [D] NAN1 weak similarity to fruit fly TFIID subunit p85 YLR129W [D] DIP2 DOM34P-interacting protein YBR247C [F] ENP1 effects N-glycosylation YDR299W [O] BFR2 involved in protein transport steps at the Brefeldin A blocks YDL148C [P] NOP14 nuclear and nucleolar protein with possible role in ribosome biogenesis YHR148W [T] IMP3 component of the U3 small nucleolar ribonucleoprotein YLL011W [T] SOF1 involved in 18S pre-rRNA production YOR061W [T] CKA2 casein kinase II alpha' chain YER127W [T] LCP5 NGG1P interacting protein | | |
| YCR057C [C] PWP2 periodic tryptophan protein YPL126W [D] NAN1 weak similarity to fruit fly TFIID subunit p85 YLR129W [D] DIP2 DOM34P-interacting protein YBR247C [F] ENP1 effects N-glycosylation YDR299W [O] BFR2 involved in protein transport steps at the Brefeldin A blocks YDL148C [P] NOP14 nuclear and nucleolar protein with possible role in ribosome biogenesis YHR148W [T] IMP3 component of the U3 small nucleolar ribonucleoprotein YLL011W [T] SOF1 involved in 18S pre-rRNA production YOR061W [T] CKA2 casein kinase II alpha' chain YER127W [T] LCP5 NGG1P interacting protein | | |
| YCR057C [C] PWP2 periodic tryptophan protein YPL126W [D] NAN1 weak similarity to fruit fly TFIID subunit p85 YLR129W [D] DIP2 DOM34P-interacting protein YBR247C [F] ENP1 effects N-glycosylation YDR299W [O] BFR2 involved in protein transport steps at the Brefeldin A blocks YDL148C [P] NOP14 nuclear and nucleolar protein with possible role in ribosome biogenesis YHR148W [T] IMP3 component of the U3 small nucleolar ribonucleoprotein YLL011W [T] SOF1 involved in 18S pre-rRNA production YOR061W [T] CKA2 casein kinase II alpha' chain YER127W [T] LCP5 NGG1P interacting protein | YNL132W | [C] KRE33 similarity to A.ambisexualis antheridiol steroid receptor |
| YLR129W [D] DIP2 DOM34P-interacting protein YBR247C [F] ENP1 effects N-glycosylation YDR299W [O] BFR2 involved in protein transport steps at the Brefeldin A blocks YDL148C [P] NOP14 nuclear and nucleolar protein with possible role in ribosome biogenesis YHR148W [T] IMP3 component of the U3 small nucleolar ribonucleoprotein YLL011W [T] SOF1 involved in 18S pre-rRNA production YOR061W [T] CKA2 casein kinase II alpha' chain YER127W [T] LCP5 NGG1P interacting protein | YCR057C | |
| YBR247C [F] ENP1 effects N-glycosylation YDR299W [O] BFR2 involved in protein transport steps at the Brefeldin A blocks YDL148C [P] NOP14 nuclear and nucleolar protein with possible role in ribosome biogenesis YHR148W [T] IMP3 component of the U3 small nucleolar ribonucleoprotein YLL011W [T] SOF1 involved in 18S pre-rRNA production YOR061W [T] CKA2 casein kinase II alpha' chain YER127W [T] LCP5 NGG1P interacting protein | YPL126W | [D] NAN1 weak similarity to fruit fly TFIID subunit p85 |
| YDR299W [O] BFR2 involved in protein transport steps at the Brefeldin A blocks YDL148C [P] NOP14 nuclear and nucleolar protein with possible role in ribosome biogenesis YHR148W [T] IMP3 component of the U3 small nucleolar ribonucleoprotein YLL011W [T] SOF1 involved in 18S pre-rRNA production YOR061W [T] CKA2 casein kinase II alpha' chain YER127W [T] LCP5 NGG1P interacting protein | YLR129W | [D] DIP2 DOM34P-interacting protein |
| YDL148C [P] NOP14 nuclear and nucleolar protein with possible role in ribosome biogenesis YHR148W [T] IMP3 component of the U3 small nucleolar ribonucleoprotein YLL011W [T] SOF1 involved in 18S pre-rRNA production YOR061W [T] CKA2 casein kinase II alpha' chain YER127W [T] LCP5 NGG1P interacting protein | YBR247C | [F] ENP1 effects N-glycosylation |
| YHR148W [T] IMP3 component of the U3 small nucleolar ribonucleoprotein YLL011W [T] SOF1 involved in 18S pre-rRNA production YOR061W [T] CKA2 casein kinase II alpha' chain YER127W [T] LCP5 NGG1P interacting protein | YDR299W | [O] BFR2 involved in protein transport steps at the Brefeldin A blocks |
| YLL011W [T] SOF1 involved in 18S pre-rRNA production YOR061W [T] CKA2 casein kinase II alpha' chain YER127W [T] LCP5 NGG1P interacting protein | YDL148C | [P] NOP14 nuclear and nucleolar protein with possible role in ribosome biogenesis |
| YOR061W [T] CKA2 casein kinase II alpha' chain YER127W [T] LCP5 NGG1P interacting protein | YHR148W | [T] IMP3 component of the U3 small nucleolar ribonucleoprotein |
| YER127W [T] LCP5 NGG1P interacting protein | YLL011W | [T] SOF1 involved in 18S pre-rRNA production |
| | YOR061W | [T] CKA2 casein kinase II alpha' chain |
| YIL035C [T] CKA1 casein kinase II, catalytic alpha chain | YER127W | [T] LCP5 NGG1P interacting protein |
| | YIL035C | [T] CKA1 casein kinase II, catalytic alpha chain |

| YOR039W | TELOVEDO : 1: H1 / 1 : |
|---|--|
| VDI 0170 | [T] CKB2 casein kinase II beta' chain |
| YPL217C | [T] BMS1 GTP-binding protein, required for distinct steps of 40S ribosome biogenesis |
| YJR002W | [T] MPP10 component of the U3 small nucleolar ribonucleoprotein |
| YGL019W | [T] CKB1 casein kinase II, beta subunit |
| YOR145C | [U] YOR145c strong similarity to hypothtical S. pombe protein and to hypothetical C. |
| YPR144C | elegans protein [U] YPR144c similarity to YDR060w and C.elegans hypothetical protein |
| | , , , , , , , , , , , , , , , , , , , |
| YLR222C YOL077C | [U] CST29 similarity to DIP2P [U] BRX1 strong similarity to C.elegans K12H4.3 protein |
| YGR090W | [U] YGR090w similarity to PIR:T40678 hypothetical protein SPBC776.08c S. pombe |
| | [U] KRE31 similarity to M.sexta steroid regulated MNG10 protein |
| YER082C | [U] EMG1 strong similarity to S.pombe hypothetical protein C18G6.07C |
| YLR186W YKR060W | [U] YKR060w similarity to hypothetical protein S. pombe |
| YLR409C | [U] YLR409c strong similarity to S. pombe beta-transducin |
| YJL069C | [U] YJL069c similarity to C.elegans hypothetical protein |
| YGR128C | [U] YGR128c hypothetical protein |
| YMR093W | [U] YMR093w weak similarity to PWP2P |
| YDR449C | [U] YDR449c similarity to hypothetical protein S. pombe |
| YHR196W | [U] YHR196w weak similarity to YDR398w |
| YJL109C | [U] YJL109c weak similarity to ATPase DRS2P |
| YKL099C | [U] YKL099c similarity to C.elegans hypothetical proteins C18G6.06 and C16C10.2 |
| YDR324C | [U] YDR324c weak similarity to beta transducin from S. pombe and other WD-40 repeat |
| TDR32+C | containing proteins |
| Q-clique 10 | Function Annotation |
| YBR283C | [F] SSH1 involved in co-translational pathway of protein transport |
| YLR378C | [O] SEC61 ER protein-translocation complex subunit |
| YDR117C | [O] YDR117c similarity to mouse ligatin, a trafficking receptor for phosphoglycoproteins |
| YGR220C | [P] MRPL9 ribosomal protein YmL9, mitochondrial |
| YMR188C | [P] YMR188c weak similarity to bacterial ribosomal protein S17 |
| YJL177W | [P] RPL17B 60s large subunit ribosomal protein L17.e |
| YDR025W | [P] RPS11A ribosomal protein S11.e |
| YDR012W | [P] RPL4B ribosomal protein L4.e.B |
| YJL190C | [P] RPS22A ribosomal protein S15a.e.c10 |
| YNL284C | [P] MRPL10 ribosomal protein of the large subunit, mitochondrial |
| MIDOOCC | [1] WIKI LTO Hoosomal protein of the large subunit, intochondral |
| YHR203C | [P] RPS4B ribosomal protein S4.e.c8 |
| YHR203C YPL131W | [P] RPS4B ribosomal protein S4.e.c8 |
| | |
| YPL131W | [P] RPS4B ribosomal protein S4.e.c8 [P] RPL5 60S large subunit ribosomal protein L5.e |
| YPL131W YOL040C | [P] RPS4B ribosomal protein S4.e.c8 [P] RPL5 60S large subunit ribosomal protein L5.e [P] RPS15 40S small subunit ribosomal protein |
| YPL131W YOL040C YER117W | [P] RPS4B ribosomal protein S4.e.c8 [P] RPL5 60S large subunit ribosomal protein L5.e [P] RPS15 40S small subunit ribosomal protein [P] RPL23B ribosomal protein L23.e |
| YPL131W YOL040C YER117W YPR102C | [P] RPS4B ribosomal protein S4.e.c8 [P] RPL5 60S large subunit ribosomal protein L5.e [P] RPS15 40S small subunit ribosomal protein [P] RPL23B ribosomal protein L23.e [P] RPL11A ribosomal protein L11.e |
| YPL131W YOL040C YER117W YPR102C YLR367W YGL103W YGL147C | [P] RPS4B ribosomal protein S4.e.c8 [P] RPL5 60S large subunit ribosomal protein L5.e [P] RPS15 40S small subunit ribosomal protein [P] RPL23B ribosomal protein L23.e [P] RPL11A ribosomal protein L11.e [P] RPS22B ribosomal protein S15a.e.c12 [P] RPL28 60S large subunit ribosomal protein L27a.e [P] RPL9A ribosomal protein L9.e |
| YPL131W YOL040C YER117W YPR102C YLR367W YGL103W | [P] RPS4B ribosomal protein S4.e.c8 [P] RPL5 60S large subunit ribosomal protein L5.e [P] RPS15 40S small subunit ribosomal protein [P] RPL23B ribosomal protein L23.e [P] RPL11A ribosomal protein L11.e [P] RPS22B ribosomal protein S15a.e.c12 [P] RPL28 60S large subunit ribosomal protein L27a.e [P] RPL9A ribosomal protein L9.e [P] RSM19 strong similarity to Mycoplasma ribosomal protein S19 |
| YPL131W YOL040C YER117W YPR102C YLR367W YGL103W YGL147C | [P] RPS4B ribosomal protein S4.e.c8 [P] RPL5 60S large subunit ribosomal protein L5.e [P] RPS15 40S small subunit ribosomal protein [P] RPL23B ribosomal protein L23.e [P] RPL11A ribosomal protein L11.e [P] RPS22B ribosomal protein S15a.e.c12 [P] RPL28 60S large subunit ribosomal protein L27a.e [P] RPL9A ribosomal protein L9.e [P] RSM19 strong similarity to Mycoplasma ribosomal protein S19 [P] RPL4A ribosomal protein |
| YPL131W YOL040C YER117W YPR102C YLR367W YGL103W YGL147C YNR037C | [P] RPS4B ribosomal protein S4.e.c8 [P] RPL5 60S large subunit ribosomal protein L5.e [P] RPS15 40S small subunit ribosomal protein [P] RPL23B ribosomal protein L23.e [P] RPL11A ribosomal protein L11.e [P] RPS22B ribosomal protein S15a.e.c12 [P] RPL28 60S large subunit ribosomal protein L27a.e [P] RPL9A ribosomal protein L9.e [P] RSM19 strong similarity to Mycoplasma ribosomal protein S19 [P] RPL4A ribosomal protein [P] RPS29B ribosomal protein S29.e.B |
| YPL131W YOL040C YER117W YPR102C YLR367W YGL103W YGL147C YNR037C YBR031W YDL061C YHR147C | [P] RPS4B ribosomal protein S4.e.c8 [P] RPL5 60S large subunit ribosomal protein L5.e [P] RPS15 40S small subunit ribosomal protein [P] RPL23B ribosomal protein L23.e [P] RPL11A ribosomal protein L11.e [P] RPS22B ribosomal protein S15a.e.c12 [P] RPL28 60S large subunit ribosomal protein L27a.e [P] RPL9A ribosomal protein L9.e [P] RSM19 strong similarity to Mycoplasma ribosomal protein S19 [P] RPL4A ribosomal protein [P] RPS29B ribosomal protein S29.e.B [P] MRPL6 ribosomal protein of the large subunit, mitochondrial |
| YPL131W YOL040C YER117W YPR102C YLR367W YGL103W YGL147C YNR037C YBR031W YDL061C YHR147C YDL191W | [P] RPS4B ribosomal protein S4.e.c8 [P] RPL5 60S large subunit ribosomal protein L5.e [P] RPS15 40S small subunit ribosomal protein [P] RPL23B ribosomal protein L23.e [P] RPL11A ribosomal protein L11.e [P] RPS22B ribosomal protein S15a.e.c12 [P] RPL28 60S large subunit ribosomal protein L27a.e [P] RPL9A ribosomal protein L9.e [P] RSM19 strong similarity to Mycoplasma ribosomal protein S19 [P] RPL4A ribosomal protein [P] RPS29B ribosomal protein S29.e.B [P] MRPL6 ribosomal protein of the large subunit, mitochondrial [P] RPL35A 60S large subunit ribosomal protein |
| YPL131W YOL040C YER117W YPR102C YLR367W YGL103W YGL147C YNR037C YBR031W YDL061C YHR147C YDL191W YGL123W | [P] RPS4B ribosomal protein S4.e.c8 [P] RPL5 60S large subunit ribosomal protein L5.e [P] RPS15 40S small subunit ribosomal protein [P] RPL23B ribosomal protein L23.e [P] RPL11A ribosomal protein L11.e [P] RPS22B ribosomal protein S15a.e.c12 [P] RPL28 60S large subunit ribosomal protein L27a.e [P] RPL9A ribosomal protein L9.e [P] RSM19 strong similarity to Mycoplasma ribosomal protein S19 [P] RPL4A ribosomal protein [P] RPS29B ribosomal protein S29.e.B [P] MRPL6 ribosomal protein of the large subunit, mitochondrial [P] RPL35A 60S large subunit ribosomal protein [P] RPS2 40S small subunit ribosomal protein |
| YPL131W YOL040C YER117W YPR102C YLR367W YGL103W YGL147C YNR037C YBR031W YDL061C YHR147C YDL191W YGL123W YBL087C | [P] RPS4B ribosomal protein S4.e.c8 [P] RPL5 60S large subunit ribosomal protein L5.e [P] RPS15 40S small subunit ribosomal protein [P] RPL23B ribosomal protein L23.e [P] RPL11A ribosomal protein L11.e [P] RPS22B ribosomal protein S15a.e.c12 [P] RPL28 60S large subunit ribosomal protein L27a.e [P] RPL9A ribosomal protein L9.e [P] RSM19 strong similarity to Mycoplasma ribosomal protein S19 [P] RPL4A ribosomal protein [P] RPS29B ribosomal protein S29.e.B [P] MRPL6 ribosomal protein of the large subunit, mitochondrial [P] RPL35A 60S large subunit ribosomal protein [P] RPS2 40S small subunit ribosomal protein [P] RPL23A 60S large subunit ribosomal protein [P] RPL23A 60S large subunit ribosomal protein |
| YPL131W YOL040C YER117W YPR102C YLR367W YGL103W YGL147C YNR037C YBR031W YDL061C YHR147C YDL191W YGL123W YBL087C YKL180W | [P] RPS4B ribosomal protein S4.e.c8 [P] RPL5 60S large subunit ribosomal protein L5.e [P] RPS15 40S small subunit ribosomal protein [P] RPL23B ribosomal protein L23.e [P] RPL11A ribosomal protein L11.e [P] RPS22B ribosomal protein S15a.e.c12 [P] RPL28 60S large subunit ribosomal protein L27a.e [P] RPL9A ribosomal protein L9.e [P] RSM19 strong similarity to Mycoplasma ribosomal protein S19 [P] RPL4A ribosomal protein [P] RPS29B ribosomal protein S29.e.B [P] MRPL6 ribosomal protein of the large subunit, mitochondrial [P] RPS2 40S small subunit ribosomal protein [P] RPS2 40S small subunit ribosomal protein [P] RPL23A 60S large subunit ribosomal protein [P] RPL23A 60S large subunit ribosomal protein L23.e [P] RPL17A ribosomal protein L17.e |
| YPL131W YOL040C YER117W YPR102C YLR367W YGL103W YGL147C YNR037C YBR031W YDL061C YHR147C YDL191W YGL123W YBL087C YKL180W YBL027W | [P] RPS4B ribosomal protein S4.e.c8 [P] RPL5 60S large subunit ribosomal protein L5.e [P] RPS15 40S small subunit ribosomal protein [P] RPL23B ribosomal protein L23.e [P] RPL11A ribosomal protein L11.e [P] RPS22B ribosomal protein S15a.e.c12 [P] RPL28 60S large subunit ribosomal protein L27a.e [P] RPL9A ribosomal protein L9.e [P] RSM19 strong similarity to Mycoplasma ribosomal protein S19 [P] RPL4A ribosomal protein [P] RPS29B ribosomal protein S29.e.B [P] MRPL6 ribosomal protein of the large subunit, mitochondrial [P] RPS2 40S small subunit ribosomal protein [P] RPS2 40S small subunit ribosomal protein [P] RPL23A 60S large subunit ribosomal protein [P] RPL17A ribosomal protein L17.e [P] RPL19B 60S large subunit ribosomal protein L19.e |
| YPL131W YOL040C YER117W YPR102C YLR367W YGL103W YGL147C YNR037C YBR031W YDL061C YHR147C YDL191W YGL123W YBL087C YKL180W YBL027W YJR145C | [P] RPS4B ribosomal protein S4.e.c8 [P] RPL5 60S large subunit ribosomal protein L5.e [P] RPS15 40S small subunit ribosomal protein [P] RPL23B ribosomal protein L23.e [P] RPL11A ribosomal protein L11.e [P] RPS22B ribosomal protein S15a.e.c12 [P] RPL28 60S large subunit ribosomal protein L27a.e [P] RPL9A ribosomal protein L9.e [P] RSM19 strong similarity to Mycoplasma ribosomal protein S19 [P] RPL4A ribosomal protein [P] RPS29B ribosomal protein S29.e.B [P] MRPL6 ribosomal protein of the large subunit, mitochondrial [P] RPS2 40S small subunit ribosomal protein [P] RPS2 40S small subunit ribosomal protein [P] RPL23A 60S large subunit ribosomal protein [P] RPL17A ribosomal protein L17.e [P] RPL19B 60S large subunit ribosomal protein L19.e [P] RPS4A ribosomal protein S4.e.c10 |
| YPL131W YOL040C YER117W YPR102C YLR367W YGL103W YGL147C YNR037C YBR031W YDL061C YHR147C YDL191W YGL123W YBL087C YKL180W YBL027W YJR145C YBR251W | [P] RPS4B ribosomal protein S4.e.c8 [P] RPL5 60S large subunit ribosomal protein L5.e [P] RPS15 40S small subunit ribosomal protein [P] RPL23B ribosomal protein L23.e [P] RPL11A ribosomal protein L11.e [P] RPS22B ribosomal protein S15a.e.c12 [P] RPL28 60S large subunit ribosomal protein L27a.e [P] RPL9A ribosomal protein L9.e [P] RSM19 strong similarity to Mycoplasma ribosomal protein S19 [P] RPL4A ribosomal protein [P] RPS29B ribosomal protein S29.e.B [P] MRPL6 ribosomal protein of the large subunit, mitochondrial [P] RPS2 40S small subunit ribosomal protein [P] RPS2 40S small subunit ribosomal protein [P] RPL23A 60S large subunit ribosomal protein [P] RPL17A ribosomal protein L17.e [P] RPL19B 60S large subunit ribosomal protein L19.e [P] RPS4A ribosomal protein S4.e.c10 [P] MRPS5 ribosomal protein S5, mitochondrial |
| YPL131W YOL040C YER117W YPR102C YLR367W YGL103W YGL147C YNR037C YBR031W YDL061C YHR147C YDL191W YGL123W YBL087C YKL180W YBL027W YJR145C | [P] RPS4B ribosomal protein S4.e.c8 [P] RPL5 60S large subunit ribosomal protein L5.e [P] RPS15 40S small subunit ribosomal protein [P] RPL23B ribosomal protein L23.e [P] RPL11A ribosomal protein L11.e [P] RPS22B ribosomal protein S15a.e.c12 [P] RPL28 60S large subunit ribosomal protein L27a.e [P] RPL9A ribosomal protein L9.e [P] RSM19 strong similarity to Mycoplasma ribosomal protein S19 [P] RPL4A ribosomal protein [P] RPS29B ribosomal protein S29.e.B [P] MRPL6 ribosomal protein of the large subunit, mitochondrial [P] RPS2 40S small subunit ribosomal protein [P] RPS2 40S small subunit ribosomal protein [P] RPL23A 60S large subunit ribosomal protein [P] RPL17A ribosomal protein L17.e [P] RPL19B 60S large subunit ribosomal protein L19.e [P] RPS4A ribosomal protein S4.e.c10 |

| YIL018W | [P] RPL2B 60S large subunit ribosomal protein L8.e |
|--------------------|---|
| YML025C | [P] YML6 ribosomal protein, mitochondrial |
| YBL092W | [P] RPL32 60S large subunit ribosomal protein L32.e |
| YBR084C-A | [P] RPL19A 60S large subunit ribosomal protein L19.e |
| YPR166C | [P] MRP2 ribosomal protein S14 |
| YDL136W | [P] RPL35B 60S large subunit ribosomal protein |
| YOR063W | [P] RPL3 60S large subunit ribosomal protein L3.e |
| YNL067W | [P] RPL9B ribosomal protein L9.e.c14 |
| YDR237W | [P] MRPL7 ribosomal protein of the large subunit, mitochondrial |
| YGR085C | [P] RPL11B ribosomal protein |
| YEL050C | [P] RML2 ribosomal L2 protein, mitochondrial |
| YGR034W | [P] RPL26B 60S large subunit ribosomal protein |
| YLR388W | [P] RPS29A ribosomal protein S29.e.A |
| YKL170W | [P] MRPL38 ribosomal protein of the large subunit (L14), mitochondrial |
| YNL244C | [P] SUI1 translation initiation factor 3 (eIF3) |
| YNL292W | [T] PUS4 pseudouridine synthase |
| YLR175W | [T] CBF5 putative rRNA pseuduridine synthase |
| YBR257W | [T] POP4 involved in processing of tRNAs and rRNAs |
| YJR014W | [U] YJR014w strong similarity to S.pombe hypothetical protein SPBC16C6.05 |
| YMR310C | [U] YMR310c similarity to YGR283c |
| YNL177C | [U] YNL177c similarity to hypothetical protein S. pombe |
| YGR283C | [U] YGR283c similarity to hypothetical protein YMR310c |
| YMR158W | [U] YMR158w weak similarity to E.coli ribosomal S8 protein |
| Q-clique 11 | Function Annotation |
| YHL030W | [C] ECM29 involved in cell wall biogenesis and architecture |
| YBR272C | [D] HSM3 mismatch repair protein |
| YOR259C | [F] RPT4 26S proteasome regulatory subunit |
| YOR117W | [F] RPT5 26S proteasome regulatory subunit |
| YFR052W | [F] RPN12 26S proteasome regulatory subunit |
| YGL011C | [F] SCL1 20S proteasome subunit YC7ALPHA/Y8 (alpha1) |
| YDR427W | [F] RPN9 subunit of the regulatory particle of the proteasome |
| YOR261C | [F] RPN8 26S proteasome regulatory subunit |
| YER012W | [F] PRE1 20S proteasome subunit C11(beta4) |
| YMR314W | [F] PRE5 20S proteasome subunit(alpha6) |
| YER021W | [F] RPN3 26S proteasome regulatory subunit |
| YDL007W | [F] RPT2 26S proteasome regulatory subunit |
| YDR394W | [F] RPT3 26S proteasome regulatory subunit |
| YFR004W | [F] RPN11 26S proteasome regulatory subunit |
| YGL048C | [F] RPT6 26S proteasome regulatory subunit |
| YPR108W | [F] RPN7 subunit of the regulatory particle of the proteasome |
| YDL147W | [F] RPN10 26S protessome regulatory garbanit |
| YHR200W | [F] RPN10 26S proteasome regulatory subunit |
| YDL097C | [F] RPN6 subunit of the regulatory particle of the proteasome |
| YKL145W | [F] RPT1 26S proteasome regulatory subunit |
| YGR232W | [F] NAS6 possible homolog of human 26S proteasome regulatory subunit p28 |
| YJR109C YKL104C | [G] CPA2 arginine-specific carbamoylphosphate synthase, large chain [M] GFA1 glucosaminefructose-6-phosphate transaminase |
| YLR421C | [U] RPN13 weak similarity to human 42K membrane glycoprotein |
| Q-clique 12 | Function Annotation |
| YML054C | [E] CYB2 lactate dehydrogenase cytochrome b2 |
| | |
| Y VIR /UX W | LIMI ERG12 mevalonate kinase |
| YMR208W YIL063C | [M] ERG12 mevalonate kinase |
| YJL063C | [P] MRPL8 ribosomal protein L17, mitochondrial |
| YJL063C YJR113C | [P] MRPL8 ribosomal protein L17, mitochondrial [P] RSM7 similarity to bacterial, chloroplast and mitochondrial ribosomal protein S7 |
| YJL063C | [P] MRPL8 ribosomal protein L17, mitochondrial |

| TYPY 110YY | |
|-------------|---|
| YPL118W | [P] MRP51 mitochondrial ribosomal protein of the small subunit |
| YML026C | [P] RPS18B ribosomal protein S18.e.c13 |
| YNL306W | [P] MRPS18 ribosomal protein of the small subunit, mitochondrial |
| YNL301C | [P] RPL18B 60S large subunit ribosomal protein L18.e |
| YOL120C | [P] RPL18A 60S large subunit ribosomal protein S18.e |
| YPL183W-A | [P] YPL183w-a strong similarity to mitochondrial and bacterial ribosomal L36 proteins |
| YDR337W | [P] MRPS28 ribosomal protein of the small subunit, mitochondrial |
| YGR084C | [P] MRP13 ribosomal protein of the small subunit, mitochondrial |
| YDR450W | [P] RPS18A ribosomal protein S18.e.c4 |
| YNL137C | [P] NAM9 ribosomal protein, mitochondrial |
| YHL004W | [P] MRP4 ribosomal protein of the small subunit, mitochondrial |
| YNL081C | [P] YNL081c similarity to ribosomal protein S13 |
| YJL191W | [P] RPS14B 40S small subunit ribosomal protein S14.e.B |
| YDR347W | [P] MRP1 ribosomal protein of the small subunit, mitochondrial |
| YDL083C | [P] RPS16B ribosomal protein S16.e |
| YMR143W | [P] RPS16A ribosomal protein S16.e |
| YNL069C | [P] RPL16B 60S large subunit ribosomal protein |
| YBL038W | [P] MRPL16 ribosomal protein of the large subunit, mitochondrial |
| YLR075W | [P] RPL10 60S large subunit ribosomal protein |
| YBR146W | [P] MRPS9 ribosomal protein S9 precursor, mitochondrial |
| YCR031C | [P] RPS14A 40S Ribosomal protein S14.e |
| YOR150W | [P] MRPL23 ribosomal protein of the large subunit, mitochondrial |
| YMR260C | [P] TIF11 translation initiation factor eIF1a |
| YIL021W | [T] RPB3 DNA-directed RNA-polymerase II, 45 kDa |
| YBR154C | [T] RPB5 DNA-directed RNA polymerase I, II, III 25 KD subunit |
| YPR110C | [T] RPC40 DNA-directed RNA polymerase I, III 40 KD subunit |
| YPR187W | [T] RPO26 DNA-directed RNA polymerase I, II, III 18 KD subunit |
| YOR116C | [T] RPO31 DNA-directed RNA polymerase III, 160 KD subunit |
| YOR207C | [T] RET1 DNA-directed RNA polymerase III, 130 KD subunit |
| YOR341W | [T] RPA190 DNA-directed RNA polymerase I, 190 KD alpha subunit |
| YOR210W | [T] RPB10 DNA-directed polymerase I, II, III 8.3 subunit |
| YDL140C | [T] RPO21 DNA-directed RNA polymerase II, 215 KD subunit |
| YPR010C | [T] RPA135 DNA-directed RNA polymerase I, 135 KD subunit |
| YIL093C | [U] RSM25 weak similarity to S.pombe hypothetical protein SPBC16A3 |
| YKL155C | [U] RSM22 similarity to S. pombe SPAC1420.04c putative cytochrome c oxidase assembly |
| VIDOOM | protein |
| YJR008W | [U] YJR008w similarity to S.pombe hypothetical protein |
| YGL129C | [U] RSM23 similarity to S.pombe hypothetical protein SPBC29A3.15C - putative |
| YDR036C | mitochondrial function [U] YDR036c similarity to enoyl CoA hydratase |
| Q-clique 13 | Function Annotation |
| YMR208W | [M] ERG12 mevalonate kinase |
| YJL063C | [P] MRPL8 ribosomal protein L17, mitochondrial |
| YPL183W-A | [P] YPL183w-a strong similarity to mitochondrial and bacterial ribosomal L36 proteins |
| YMR260C | [P] TIF11 translation initiation factor eIF1a |
| YBL038W | [P] MRPL16 ribosomal protein of the large subunit, mitochondrial |
| YLR075W | [P] RPL10 60S large subunit ribosomal protein |
| YCR031C | [P] RPS14A 40S Ribosomal protein S14.e |
| YDR450W | [P] RPS18A ribosomal protein S18.e.c4 |
| YNL081C | [P] YNL081c similarity to ribosomal protein S13 |
| YJR123W | [P] RPS5 ribosomal protein S5.e |
| YJL191W | [P] RPS14B 40S small subunit ribosomal protein S14.e.B |
| YML009C | [P] MRPL39 60S ribosomal protein, mitochondrial |
| YML026C | [P] RPS18B ribosomal protein S18.e.c13 |
| YGL068W | [P] YGL068w strong similarity to Cricetus mitochrondial ribosomal L12 protein |
| 1 32000 11 | [1] 1 02000 m strong similarly to effection intochronical fittosonial E12 protein |

| YOL120C | [P] RPL18A 60S large subunit ribosomal protein S18.e |
|-------------|--|
| YNL301C | [P] RPL18B 60S large subunit ribosomal protein L18.e |
| YNR003C | [T] RPC34 DNA-directed RNA polymerase III, 34 KD subunit |
| YOR210W | [T] RPB10 DNA-directed polymerase I, II, III 8.3 subunit |
| YPR190C | [T] RPC82 DNA-directed RNA polymerase III, 82 KD subunit |
| YPR187W | [T] RPO26 DNA-directed RNA polymerase I, II, III 18 KD subunit |
| YIL021W | [T] RPB3 DNA-directed RNA-polymerase II, 45 kDa |
| YPR110C | [T] RPC40 DNA-directed RNA polymerase I, III 40 KD subunit |
| YOR341W | [T] RPA190 DNA-directed RNA polymerase I, 190 KD alpha subunit |
| YDL140C | [T] RPO21 DNA-directed RNA polymerase II, 215 KD subunit |
| YBR154C | [T] RPB5 DNA-directed RNA polymerase I, II, III 25 KD subunit |
| YOR116C | [T] RPO31 DNA-directed RNA polymerase III, 160 KD subunit |
| YOR151C | [T] RPB2 DNA-directed RNA polymerase II, 140 kDa chain |
| YPR010C | [T] RPA135 DNA-directed RNA polymerase I, 135 KD subunit |
| YOR207C | [T] RET1 DNA-directed RNA polymerase III, 130 KD subunit |
| YOR224C | [T] RPB8 DNA-directed RNA polymerase I, II, III 16 KD subunit |
| YML010W | [T] SPT5 transcription elongation protein |
| YJR008W | [U] YJR008w similarity to S.pombe hypothetical protein |
| Q-clique 14 | Function Annotation |
| YIL147C | [C] SLN1 two-component signal transducer |
| YMR262W | [D] YMR262w similarity to S.pombe scn1 protein |
| YGL205W | [E] POX1 acyl-CoA oxidase |
| YAL054C | [E] ACS1 acetyl-CoA synthetase |
| YER061C | [E] CEM1 beta-keto-acyl-ACP synthase, mitochondrial |
| YLR153C | [E] ACS2 acetyl-coenzyme A synthetase |
| YIL160C | [E] POT1 acetyl-CoA C-acyltransferase, peroxisomal |
| YHR208W | [G] BAT1 branched chain amino acid aminotransferase, mitochondrial |
| YIL042C | [G] YIL042c similarity to rat branched-chain alpha-ketoacid dehydrogenase kinase |
| YJR148W | [G] BAT2 branched chain amino acid aminotransferase, cytosolic |
| YBR222C | [M] FAT2 AMP-binding protein, peroxisomal |
| YBR208C | [M] DUR1,2 urea amidolyase |
| YOR221C | [M] MCT1 malonyl-CoA:ACP transferase |
| YPL231W | [M] FAS2 fatty-acyl-CoA synthase, alpha chain |
| YPL028W | [M] ERG10 acetyl-CoA C-acetyltransferase, cytosolic |
| YDR272W | [M] GLO2 glyoxalase II (hydroxyacylglutathione hydrolase) |
| YLR284C | [M] ECI1 delta3-cis-delta2-trans-enoyl-CoA isomerase |
| YJR057W | [M] CDC8 dTMP kinase |
| YDL168W | [M] SFA1 long-chain alcohol dehydrogenase |
| YKL182W | [M] FAS1 fatty-acyl-CoA synthase, beta chain |
| YNR016C | [M] ACC1 acetyl-CoA carboxylase |
| YKL192C | [M] ACP1 mitochonrial acyl-carrier protein |
| YOR180C | [M] DCI1 Enoyl-CoA Hydratase, peroxisomal |
| YBR041W | [M] FAT1 very long-chain fatty acyl-CoA synthetase |
| YOR040W | [M] GLO4 glyoxalase II (hydroxyacylglutathione hydrolase) |
| YKR009C | [M] FOX2 hydratase-dehydrogenase-epimerase, peroxisomal |
| YCR003W | [P] MRPL32 ribosomal protein YmL32, mitochondrial |
| YNL168C | [U] YNL168c similarity to C.elegans ZK688.3 protein and E.coli hpcEp |
| YGL059W | [U] YGL059w similarity to rat branched-chain alpha-ketoacid dehydrogenase kinase |
| YGR263C | [U] YGR263c weak similarity to E.coli lipase like enzyme |
| YDR036C | [U] YDR036c similarity to enoyl CoA hydratase |
| YDR428C | [U] YDR428c weak similarity to predicted esterase of proteobacterium |
| YOR093C | [U] YOR093c similarity to S.pombe hypothetical protein SPAC22F3.04 |
| YBL055C | [U] YBL055c similarity to hypothetical S.pombe protein |
| Q-clique 15 | Function Annotation |
| YOL142W | [D] RRP40 protein involved in ribosomal RNA processing, component of the exosome |

| | complex responsible for 3'end processing and degradation of many RNA species |
|-------------|---|
| YNL232W | [M] CSL4 core component of the 3'-5' exosome |
| YOR076C | [M] CSL4 core component of the 3-3 exosome [M] SKI7 GTPase with function in 3'-to-5' degradation of mRNA |
| | · · |
| YNL189W | [O] SRP1 karyopherin-alpha or importin |
| YLR029C | [P] RPL15A 60s large subunit ribosomal protein L15.e.c12 |
| YPR043W | [P] RPL43A ribosomal protein L37a.e |
| YMR121C | [P] RPL15B 60S large subunit ribosomal protein L15.e.c13 |
| YDL111C | [T] RRP42 rRNA processing protein |
| YOL021C | [T] DIS3 3'->5' exoribonuclease required for 3' end formation of 5.8S rRNA |
| YCR035C | [T] RRP43 rRNA processing protein |
| YHR062C | [T] RPP1 required for processing of tRNA and 35S rRNA |
| YGR195W | [T] SKI6 3'->5' exoribonuclease required for 3' end formation of 5.8S rRNA |
| YNL075W | [T] IMP4 component of the U3 small nucleolar ribonucleoprotein |
| YAL033W | [T] POP5 required for processing of tRNAs and rRNAs |
| YGR158C | [T] MTR3 involved in mRNA transport |
| YDR280W | [T] RRP45 rRNA processing protein |
| YGR095C | [T] RRP46 involved in rRNA processing |
| YHR069C | [T] RRP4 3'->5' exoribonuclease required for 3' end formation of 5.8S rRNA |
| YOR001W | [U] RRP6 similarity to human nucleolar 100K polymyositis-scleroderma protein |
| YLR022C | [U] YLR022c similarity to C.elegans and M.jannaschii hypothetical proteins |
| YHR088W | [U] RPF1 similarity to hypothetical protein YNL075w |
| Q-clique 16 | Function Annotation |
| YIL147C | [C] SLN1 two-component signal transducer |
| YMR262W | [D] YMR262w similarity to S.pombe scn1 protein |
| YLR153C | [E] ACS2 acetyl-coenzyme A synthetase |
| YIL160C | [E] POT1 acetyl-CoA C-acyltransferase, peroxisomal |
| YGL205W | [E] POX1 acyl-CoA oxidase |
| YER061C | [E] CEM1 beta-keto-acyl-ACP synthase, mitochondrial |
| YIL042C | [G] YIL042c similarity to rat branched-chain alpha-ketoacid dehydrogenase kinase |
| YJR148W | [G] BAT2 branched chain amino acid aminotransferase, cytosolic |
| YHR208W | [G] BAT1 branched chain amino acid aminotransferase, mitochondrial |
| YOR180C | [M] DCI1 Enoyl-CoA Hydratase, peroxisomal |
| YKR009C | [M] FOX2 hydratase-dehydrogenase-epimerase, peroxisomal |
| YBR222C | [M] FAT2 AMP-binding protein, peroxisomal |
| YBR208C | [M] DUR1,2 urea amidolyase |
| YOR221C | [M] MCT1 malonyl-CoA:ACP transferase |
| YPL231W | [M] FAS2 fatty-acyl-CoA synthase, alpha chain |
| YPL028W | [M] ERG10 acetyl-CoA C-acetyltransferase, cytosolic |
| YJR057W | [M] CDC8 dTMP kinase |
| YDL168W | [M] SFA1 long-chain alcohol dehydrogenase |
| YLR284C | [M] ECI1 delta3-cis-delta2-trans-enoyl-CoA isomerase |
| YKL182W | [M] FAS1 fatty-acyl-CoA synthase, beta chain |
| YNR016C | [M] ACC1 acetyl-CoA carboxylase |
| YKL192C | [M] ACP1 mitochonrial acyl-carrier protein |
| YBR041W | [M] FAT1 very long-chain fatty acyl-CoA synthetase |
| YJR149W | [M] YJR149w similarity to 2-nitropropane dioxygenase |
| YCR003W | [P] MRPL32 ribosomal protein YmL32, mitochondrial |
| YGR263C | [U] YGR263c weak similarity to E.coli lipase like enzyme |
| YDR036C | [U] YDR036c similarity to enoyl CoA hydratase |
| YGL059W | [U] YGL059w similarity to rat branched-chain alpha-ketoacid dehydrogenase kinase |
| YDR428C | [U] YDR428c weak similarity to predicted esterase of proteobacterium |
| YBL055C | [U] YBL055c similarity to hypothetical S.pombe protein |
| YOR093C | [U] YOR093c similarity to S.pombe hypothetical protein SPAC22F3.04 |
| Q-clique 17 | Function Annotation |
| YGR245C | [D] SDA1 required for normal organization of the actin cytoskeleton; required for passage |

| hrough Start YFR006W [O] YFR006w similarity to P.polycephalum myosin-related protein mlpA YOR206W [O] NOC2 crucial for intranuclear movement of ribosomal precursor particles YPR016C [P] TIF6 translation initiation factor 6 (eIF6) YNL061W [T] NOP2 nucleolar protein YKL009W [T] MR74 mRNA turnover 4 YKL009W [T] MR74 mRNA biclase of the DEAD box family YL10.08W [T] DRS1 fRNA helicase of the DEAD box family YDL031W [T] DRS1 fRNA helicase of the DEAD box family YDL031W [T] DRS1 fRNA helicase of the DEAD box family YDL031W [T] DRS1 fRNA helicase involved in ribosome biogenesis YNL182C [U] YNL182c weak similarity to S.pombe hypothetical protein YNL182C [U] YLR106c similarity to Kaposis sarcoma-associated herpes-like virus ORF73 homolog gene YHR052W [U] CIC1 adaptor protein specifically linking the 26S proteasome to its substrate, the SCF component CDC4 YPL093W [U] NGG1 similarity to M.jamaschii GTP-binding protein YRR010W [U] YGR090w similarity to INR:T40678 hypothetical protein SPBC776.08c S. pombe YFR010W [U] LOC1 weak similarity to praint in SPP41P YNL002C [U] RLP3 strong similarity to to mammalian ribosomal L7 proteins YRR010W [U] RSP13 similarity to be partish in SPP41P YNL100C [U] WRR13 similarity to zebrafish essential for embryonic development gene pescadillo YNL110C [U] YNL110C [U] YNL101 weak similarity to human zinc finger protein YGR103W [U] RSR1 strong similarity to hypothetical protein S. pombe YGL077C [U] RSR1 strong similarity to hypothetical protein S. pombe YGL077C [U] RSR1 strong similarity to hypothetical protein S. pombe YRR049C [U] FRSI weak similarity to protiferation-associated protein YDR101C [U] YNR101c weak similarity to protiferation-associated protein YRR081C [U] PUR6 similarity to prothetical duman and Celegans proteins YKR081C [U] PUR6 similarity to prothetical duman and Celegans proteins YRR081C [U] PUR6 similarity to prothetical protein S. pombe YRR178W [U] YHR197w weak similarity to PUR7:22172 bypothetical protein F44E5.2 C. elegans YRR187W [U] YHR197 weak similarity to PUR7:22172 bypo | | |
|--|-------------|--|
| FORE206W IO NOC2 crucial for intranuclear movement of ribosomal precursor particles | TIED OO STI | |
| YPRO16C | | |
| YNL061W | | |
| TJ MR14 mRNA turnover 4 | | |
| YELLONSW | | |
| YDL031W T] LHP1 RNA binding protein | | |
| YDL031W | | |
| YNL182C [U] YNL182c weak similarity to Kaposi's sarcoma-associated herpes-like virus ORF73 homolog gene YHR052W [U] CIC1 adaptor protein specifically linking the 26S proteasome to its substrate, the SCF component CDC4 YPL093W [U] NOG1 similarity to M.jannaschii GTP-binding protein YGR090W [U] YGR090w similarity to PIR.740678 hypothetical protein SPBC776.08c S. pombe YFR001W [U] LOC1 weak similarity to ablit tradin SPP41P NNL00C [U] RLP7 strong similarity to mammalian ribosomal L7 proteins YLR074C [U] BUD20 weak similarity to human zinc finger protein YGR103W [U] RN13 similarity to zebrafish essential for embryonic development gene pescadillo NNL10C [U] YNL110c weak similarity to fruit fly RNA-binding protein YGL111W [U] YGL111w weak similarity to fruit fly RNA-binding protein YGL111W [U] YGL111w weak similarity to Poliferation-associated protein YGL077C [U] BRN1 strong similarity to Loclegans K12H4.3 protein YMR049C [U] ERB1 weak similarity to Drolferation-associated protein YDR101C [U] YDR101c weak similarity to proliferation-associated protein YDR496C [U] PUF6 similarity to hypothetical protein S. pombe YHR197W [U] YHR197w weak similarity to Pire.722172 hypothetical protein F44E5.2 C. elegans YER126C [U] KRE32 weak similarity to Ecoli colicin N Q-clique 18 Function Annotation YDR195W [I] SSU72 suppressor of cs mutant of SUA7 YER133W [C] GLC7 ser/thr phosphoprotein phosphatase 1, catalytic chain YDR195W [I] REP2 RNA 3'-end formation protein YDR195W [I] FNA14 component of pre-mRNA 3'-end processing factor CF II YDR301W [I] FNA14 component of pre-mRNA 3'-end processing factor CF II YDR301W [I] FNA14 component of pre-mRNA 3'-end processing factor CF II YDR301W [I] PA1 pre-tRNA processing protein /PF i subunit YRR003C [I] FPF1 component of pre-mRNA 3'-end processing factor CF II YDR303C [I] FPF1 component of pre-mRNA 3'-end processing factor CF II YDR307C [I] YSH1 component of pre-mRNA 3'-end processing factor CF II YPR107C [I] YSH1 component of pre-mRNA 3'-end processing factor CF II YPR107C [I] YSH1 component of | YDL051W | |
| YLR106C [U] YLR106c similarity to Kaposi's sarcoma-associated herpes-like virus ORF73 homolog gene YHR052W [U] CICI adaptor protein specifically linking the 26S proteasome to its substrate, the SCF component CDC4 YPL093W [U] NOG1 similarity to M.jannaschii GTP-binding protein YGR090W [U] YGR090w similarity to PIR:740678 hypothetical protein SPBC776.08c S. pombe YFR001W [U] LOC1 weak similarity to present protein SPBC776.08c S. pombe YFR001W [U] LOC1 weak similarity to mammalian ribosomal L7 proteins YRR074C [U] BUD20 weak similarity to human zinc finger protein YGR103W [U] RRP13 similarity to zebrafish essential for embryonic development gene pescadillo NNL110C [U] YNL110c weak similarity to fruit fly RNA-binding protein YGR101W [U] YGL111w weak similarity to fruit fly RNA-binding protein YGR101C [U] YNL110c weak similarity to Athaliana PRL1 protein YDR101C [U] YBR101c weak similarity to Athaliana PRL1 protein YDR101C [U] YDR101c weak similarity to Proliferation-associated protein YDR396C [U] YER081c strong similarity to proliferation-associated protein YDR396C [U] YHR197w weak similarity to PIR:722172 hypothetical protein F44E5.2 C. elegans YER126C [U] YKR081c strong similarity to PIR:722172 hypothetical protein F44E5.2 C. elegans YER126C [U] YKR032 weak similarity to PIR:722172 hypothetical protein F44E5.2 C. elegans YER128C [U] KRE32 weak similarity to Ecoli colicin N Poclique 1B SU772 suppressor of cs mutant of SUA7 YER133W [C] GLC7 ser/thr phosphoprotein phosphatase 1, catalytic chain YDR195W [T] RFE7 RNA 3'-end formation protein YMR061W [T] RNA14 component of pre-mRNA 3'-end processing factor CF1 YDR301W [T] FFR PRNA 3'-end formation protein YR093C [T] FFII pre-mRNA 3'-end processing factor CF1 YNL317W [T] PFS2 polyadenylation factor I subunit 2 required for mRNA 3'-end processing, bridges two mRNA 3'-end processing factors YLR15W [T] FFS2 polyadenylation factor I subunit 2 required for mRNA 3'-end processing, bridges two mRNA 3'-end processing complex YLR15W [T] FFS2 polyadenylation factor I subunit 2 re | YDL031W | [T] DBP10 putative RNA helicase involved in ribosome biogenesis |
| YHR052W [U] CIC1 adaptor protein specifically linking the 26S proteasome to its substrate, the SCF component CDC4 YPI.093W [U] NGGI similarity to M.jannaschii GTP-binding protein YGR090W [U] YGR090w similarity to PIR:T40678 hypothetical protein SPBC776.08c S. pombe YFR001W [U] LOC1 weak similarity to rabbit triadin SPP41P YNL002C [U] RLP7 strong similarity to rabbit triadin SPP41P YNL002C [U] RLP3 strong similarity to human zinc finger protein YGR103W [U] RRP13 similarity to zebrafish essential for embryonic development gene pescadillo YNL110C [U] YNL110c weak similarity to hypothetical protein S. pombe YOL077C [U] BRX1 strong similarity to C.elegans K12H4.3 protein YGR101W [U] YGL111W weak similarity to Pubphetical protein S. pombe YOL077C [U] BRX1 strong similarity to C.elegans K12H4.3 protein YMR049C [U] YER81 weak similarity to A.thaliana PRL1 protein YDR101C [U] YPR010 weak similarity to Pubphetical protein S. pombe YUR197W [U] YHR191C weak similarity to Pubphetical protein S. pombe YKR081C [U] YYR081c strong similarity to hypothetical protein S. pombe YHR197W [U] YHR197W weak similarity to Pubphetical protein S. pombe YPR126C [U] KRE32 weak similarity to E.coli colicin N Q-clique 18 YBR128 [SU72 suppressor of cs mutant of SUA7 YER133W [C] GLC7 ser/thr phosphoprotein phosphatase 1, catalytic chain YDR195W [T] REF2 RNA 3'-end formation protein YMR061W [T] RNA14 component of pre-mRNA 3'-end processing factor CF I YDR301W [T] CFT1 pre-mRNA 3'-end processing factor CF II YDR301W [T] CFT1 pre-mRNA 3'-end processing factor CF II YDR301W [T] CFT1 component of pre-mRNA polyadenylation factor PF I YDR302C [T] PPA1 poly(A) polymerase YLR0782C [T] PFA1 pre-tRNA processing protein / PF I subunit T CFT2 cleavage and polyadenylation specificity factor, part of CF II YPR13TW [T] PFS2 polyadenylation factor F I YDR303C [T] PFA1 pre-tRNA processing complex YLR15W [T] CFT1 component of pre-mRNA polyadenylation factor CF I YNL317W [T] PFS2 polyadenylation factor F I YPR107C [T] YH11 protein of the 3' processing complex YLR27 | YNL182C | |
| VPL093W | YLR106C | [U] YLR106c similarity to Kaposi's sarcoma-associated herpes-like virus ORF73 homolog |
| component CDC4 YPL093W [U] NOG1 similarity to M,jannaschii GTP-binding protein YGR090W [U] KOG090w similarity to PIR:T40678 hypothetical protein SPBC776.08c S. pombe YFR001W [U] LOC1 weak similarity to rabbit triadin SPP41P YNL002C [U] RLP7 strong similarity to mammalian ribosomal L7 proteins YLR074C [U] BUD20 weak similarity to brana zinc finger protein YGR103W [U] RRP13 similarity to zebrafish essential for embryonic development gene pescadillo YNL110C [U] YNL110c weak similarity to fruit fly RNA-binding protein YGL111W [U] YGL111w weak similarity to Truit fly RNA-binding protein YGL111W [U] YGL111w weak similarity to Truit fly RNA-binding protein YGL111W [U] YGL111w weak similarity to C.elegans K12H4.3 protein YMR049C [U] ERB1 weak similarity to A.thaliana PRL1 protein YDR101C [U] YDR101c weak similarity to proliferation-associated protein YDR496C [U] PUF6 similarity to hypothetical protein S. pombe YKR081C [U] YKR081c strong similarity to proliferation-associated protein YHR197W [U] YHR197w weak similarity to PIR:T22172 hypothetical protein F44E5.2 C. elegans YER126C [U] KRE32 weak similarity to E.coli colicin N YNL222W [B] SSU72 suppressor of cs mutant of SUA7 YER133W [C] GLC7 ser/thr phosphoprotein phosphatase 1, catalytic chain YDR195W [T] REF2 RNA 3'-end formation protein YMR061W [T] RNA14 component of pre-mRNA 3'-end processing factor CF I YAL043C [T] FTA1 pre-tRNA processing protein / PF I subunit YKR002W [T] PAP1 poly(A) polymerase TJF1P1 component of pre-mRNA 3'-end processing factor CF I YDR228C [T] FCF11 component of pre-mRNA 3'-end processing factor CF I YDR28C [T] PYE11 component of pre-mRNA 3'-end processing factor CF I YPR107C [T] YTH1 protein of the 3' processing complex YLR175W [T] CFT2 cleavage and polyadenylation specificity factor, part of CF II YPR107C [T] YTH1 protein of the 3' processing complex YLR175W [T] CFT2 cleavage and polyadenylation specificity factor, part of CF II YPR107C [T] YTH1 protein of the 3' processing complex YLR15W [U] SWD25 similarity to C.elegans hypothetical prote | | |
| VPL093W | YHR052W | [U] CIC1 adaptor protein specifically linking the 26S proteasome to its substrate, the SCF |
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| YNL222W [B] SSU72 suppressor of cs mutant of SUA7 YER133W [C] GLC7 ser/thr phosphoprotein phosphatase 1, catalytic chain YDR195W [T] REF2 RNA 3'-end formation protein YMR061W [T] RNA14 component of pre-mRNA 3'-end processing factor CF I YDR301W [T] CFT1 pre-mRNA 3'-end processing factor CF II YAL043C [T] PTA1 pre-tRNA processing protein / PF I subunit YKR002W [T] AP1 poly(A) polymerase YJR093C [T] FIP1 component of pre-mRNA 3'-end processing factor CF I YNL317W [T] PFS2 polyadenylation factor I subunit 2 required for mRNA 3'-end processing, bridges two mRNA 3'-end processing factors YLR115W [T] CFT2 cleavage and polyadenylation specificity factor, part of CF II YPR107C [T] YTH1 protein of the 3' processing complex YLR277C [T] YSH1 component of pre-mRNA polyadenylation factor PF I YGR156W [U] PTI1 weak similarity to PIR:A40220 cleavage stimulation factor 64K chain - human YKL059C [U] YKL059c similarity to C.elegans hypothetical protein YKL018W [U] SWD2 similarity to C.elegans hypothetical protein YKL018W [U] SWD2 similarity to C.elegans hypothetical protein YML054C [E] CYB2 lactate dehydrogenase cytochrome b2 YMR208W [M] ERG12 mevalonate kinase YLR048W [P] RPS0B 40S ribosomal protein p40 homolog B YPL118W [P] MRPS1 mitochondrial ribosomal protein of the small subunit YDR337W [P] MRPS28 ribosomal protein of the small subunit, mitochondrial | YER126C | [U] KRE32 weak similarity to E.coli colicin N |
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| YDR195W [T] REF2 RNA 3'-end formation protein YMR061W [T] RNA14 component of pre-mRNA 3'-end processing factor CF I YDR301W [T] CFT1 pre-mRNA 3'-end processing factor CF II YAL043C [T] PTA1 pre-tRNA processing protein / PF I subunit YKR002W [T] PAP1 poly(A) polymerase YJR093C [T] FIP1 component of pre-mRNA polyadenylation factor PF I YDR228C [T] PCF11 component of pre-mRNA 3'-end processing factor CF I YNL317W [T] PFS2 polyadenylation factor I subunit 2 required for mRNA 3'-end processing, bridges two mRNA 3'-end processing factors YLR115W [T] CFT2 cleavage and polyadenylation specificity factor, part of CF II YPR107C [T] YTH1 protein of the 3' processing complex YLR277C [T] YSH1 component of pre-mRNA polyadenylation factor PF I YGR156W [U] PTI1 weak similarity to PIR:A40220 cleavage stimulation factor 64K chain - human YKL059C [U] YKL059c similarity to C.elegans hypothetical protein YKL018W [U] SWD2 similarity to C.elegans hypothetical protein Q-clique 19 Function Annotation YML054C [E] CYB2 lactate dehydrogenase cytochrome b2 YMR208W [M] ERG12 mevalonate kinase YLR048W [P] RPS0B 40S ribosomal protein p40 homolog B YPL118W [P] MRPS1 mitochondrial ribosomal protein of the small subunit YDR337W [P] MRPS28 ribosomal protein of the small subunit, mitochondrial | YNL222W | [B] SSU72 suppressor of cs mutant of SUA7 |
| YMR061W[T] RNA14 component of pre-mRNA 3'-end processing factor CF IYDR301W[T] CFT1 pre-mRNA 3'-end processing factor CF IIYAL043C[T] PTA1 pre-tRNA processing protein / PF I subunitYKR002W[T] PAP1 poly(A) polymeraseYJR093C[T] FIP1 component of pre-mRNA polyadenylation factor PF IYDR228C[T] PCF11 component of pre-mRNA 3'-end processing factor CF IYNL317W[T] PFS2 polyadenylation factor I subunit 2 required for mRNA 3'-end processing, bridges two mRNA 3'-end processing factorsYLR115W[T] CFT2 cleavage and polyadenylation specificity factor, part of CF IIYPR107C[T] YTH1 protein of the 3' processing complexYLR277C[T] YSH1 component of pre-mRNA polyadenylation factor PF IYGR156W[U] PTI1 weak similarity to PIR:A40220 cleavage stimulation factor 64K chain - humanYKL059C[U] YKL059c similarity to C.elegans hypothetical proteinYKL018W[U] SWD2 similarity to C.elegans hypothetical proteinQ-clique 19Function AnnotationYML054C[E] CYB2 lactate dehydrogenase cytochrome b2YMR208W[M] ERG12 mevalonate kinaseYLR048W[P] RPS0B 40S ribosomal protein p40 homolog BYPL118W[P] MRPS1 mitochondrial ribosomal protein of the small subunitYDR337W[P] MRPS2 ribosomal protein of the small subunit, mitochondrialYBR146W[P] MRPS9 ribosomal protein of the small subunit, mitochondrial | YER133W | [C] GLC7 ser/thr phosphoprotein phosphatase 1, catalytic chain |
| YDR301W[T] CFT1 pre-mRNA 3'-end processing factor CF IIYAL043C[T] PTA1 pre-tRNA processing protein / PF I subunitYKR002W[T] PAP1 poly(A) polymeraseYJR093C[T] FIP1 component of pre-mRNA polyadenylation factor PF IYDR228C[T] PCF11 component of pre-mRNA 3'-end processing factor CF IYNL317W[T] PFS2 polyadenylation factor I subunit 2 required for mRNA 3'-end processing, bridges two mRNA 3'-end processing factorsYLR115W[T] CFT2 cleavage and polyadenylation specificity factor, part of CF IIYPR107C[T] YTH1 protein of the 3' processing complexYLR277C[T] YSH1 component of pre-mRNA polyadenylation factor PF IYGR156W[U] PTI1 weak similarity to PIR:A40220 cleavage stimulation factor 64K chain - humanYKL059C[U] YKL059c similarity to C.elegans hypothetical proteinYKL018W[U] SWD2 similarity to C.elegans hypothetical proteinYML054C[E] CYB2 lactate dehydrogenase cytochrome b2YMR208W[M] ERG12 mevalonate kinaseYLR048W[P] RPS0B 40S ribosomal protein p40 homolog BYPL118W[P] MRP51 mitochondrial ribosomal protein of the small subunitYDR337W[P] MRPS28 ribosomal protein of the small subunit, mitochondrialYBR146W[P] MRPS9 ribosomal protein S9 precursor, mitochondrial | YDR195W | |
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| YJR093C [T] FIP1 component of pre-mRNA polyadenylation factor PF I YDR228C [T] PCF11 component of pre-mRNA 3'-end processing factor CF I YNL317W [T] PFS2 polyadenylation factor I subunit 2 required for mRNA 3'-end processing, bridges two mRNA 3'-end processing factors YLR115W [T] CFT2 cleavage and polyadenylation specificity factor, part of CF II YPR107C [T] YTH1 protein of the 3' processing complex YLR277C [T] YSH1 component of pre-mRNA polyadenylation factor PF I YGR156W [U] PTI1 weak similarity to PIR:A40220 cleavage stimulation factor 64K chain - human YKL059C [U] YKL059c similarity to C.elegans hypothetical protein YKL018W [U] SWD2 similarity to C.elegans hypothetical protein Q-clique 19 Function Annotation YML054C [E] CYB2 lactate dehydrogenase cytochrome b2 YMR208W [M] ERG12 mevalonate kinase YLR048W [P] RPS0B 40S ribosomal protein p40 homolog B YPL118W [P] MRP51 mitochondrial ribosomal protein of the small subunit YDR337W [P] MRPS28 ribosomal protein of the small subunit, mitochondrial YBR146W [P] MRPS9 ribosomal protein S9 precursor, mitochondrial | YAL043C | [T] PTA1 pre-tRNA processing protein / PF I subunit |
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| YLR115W [T] CFT2 cleavage and polyadenylation specificity factor, part of CF II YPR107C [T] YTH1 protein of the 3' processing complex YLR277C [T] YSH1 component of pre-mRNA polyadenylation factor PF I YGR156W [U] PTI1 weak similarity to PIR:A40220 cleavage stimulation factor 64K chain - human YKL059C [U] YKL059c similarity to C.elegans hypothetical protein YKL018W [U] SWD2 similarity to C.elegans hypothetical protein Q-clique 19 Function Annotation YML054C [E] CYB2 lactate dehydrogenase cytochrome b2 YMR208W [M] ERG12 mevalonate kinase YLR048W [P] RPS0B 40S ribosomal protein p40 homolog B YPL118W [P] MRP51 mitochondrial ribosomal protein of the small subunit YDR337W [P] MRPS28 ribosomal protein of the small subunit, mitochondrial YBR146W [P] MRPS9 ribosomal protein S9 precursor, mitochondrial | YNL317W | |
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| YLR277C [T] YSH1 component of pre-mRNA polyadenylation factor PF I YGR156W [U] PTI1 weak similarity to PIR:A40220 cleavage stimulation factor 64K chain - human YKL059C [U] YKL059c similarity to C.elegans hypothetical protein YKL018W [U] SWD2 similarity to C.elegans hypothetical protein Punction Annotation YML054C [E] CYB2 lactate dehydrogenase cytochrome b2 YMR208W [M] ERG12 mevalonate kinase YLR048W [P] RPS0B 40S ribosomal protein p40 homolog B YPL118W [P] MRP51 mitochondrial ribosomal protein of the small subunit YDR337W [P] MRPS28 ribosomal protein of the small subunit, mitochondrial YBR146W [P] MRPS9 ribosomal protein S9 precursor, mitochondrial | | |
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| YKL059C [U] YKL059c similarity to C.elegans hypothetical protein YKL018W [U] SWD2 similarity to C.elegans hypothetical protein Q-clique 19 Function Annotation YML054C [E] CYB2 lactate dehydrogenase cytochrome b2 YMR208W [M] ERG12 mevalonate kinase YLR048W [P] RPS0B 40S ribosomal protein p40 homolog B YPL118W [P] MRP51 mitochondrial ribosomal protein of the small subunit YDR337W [P] MRPS28 ribosomal protein of the small subunit, mitochondrial YBR146W [P] MRPS9 ribosomal protein S9 precursor, mitochondrial | | |
| YKL018W [U] SWD2 similarity to C.elegans hypothetical protein Q-clique 19 Function Annotation YML054C [E] CYB2 lactate dehydrogenase cytochrome b2 YMR208W [M] ERG12 mevalonate kinase YLR048W [P] RPS0B 40S ribosomal protein p40 homolog B YPL118W [P] MRP51 mitochondrial ribosomal protein of the small subunit YDR337W [P] MRPS28 ribosomal protein of the small subunit, mitochondrial YBR146W [P] MRPS9 ribosomal protein S9 precursor, mitochondrial | | · · · |
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| YML054C [E] CYB2 lactate dehydrogenase cytochrome b2 YMR208W [M] ERG12 mevalonate kinase YLR048W [P] RPS0B 40S ribosomal protein p40 homolog B YPL118W [P] MRP51 mitochondrial ribosomal protein of the small subunit YDR337W [P] MRPS28 ribosomal protein of the small subunit, mitochondrial YBR146W [P] MRPS9 ribosomal protein S9 precursor, mitochondrial | YKL018W | [U] SWD2 similarity to C.elegans hypothetical protein |
| YMR208W[M] ERG12 mevalonate kinaseYLR048W[P] RPS0B 40S ribosomal protein p40 homolog BYPL118W[P] MRP51 mitochondrial ribosomal protein of the small subunitYDR337W[P] MRPS28 ribosomal protein of the small subunit, mitochondrialYBR146W[P] MRPS9 ribosomal protein S9 precursor, mitochondrial | Q-clique 19 | |
| YLR048W [P] RPS0B 40S ribosomal protein p40 homolog B YPL118W [P] MRP51 mitochondrial ribosomal protein of the small subunit YDR337W [P] MRPS28 ribosomal protein of the small subunit, mitochondrial YBR146W [P] MRPS9 ribosomal protein S9 precursor, mitochondrial | YML054C | [E] CYB2 lactate dehydrogenase cytochrome b2 |
| YPL118W [P] MRP51 mitochondrial ribosomal protein of the small subunit YDR337W [P] MRPS28 ribosomal protein of the small subunit, mitochondrial YBR146W [P] MRPS9 ribosomal protein S9 precursor, mitochondrial | YMR208W | [M] ERG12 mevalonate kinase |
| YDR337W [P] MRPS28 ribosomal protein of the small subunit, mitochondrial YBR146W [P] MRPS9 ribosomal protein S9 precursor, mitochondrial | YLR048W | [P] RPS0B 40S ribosomal protein p40 homolog B |
| YBR146W [P] MRPS9 ribosomal protein S9 precursor, mitochondrial | YPL118W | [P] MRP51 mitochondrial ribosomal protein of the small subunit |
| | YDR337W | [P] MRPS28 ribosomal protein of the small subunit, mitochondrial |
| YNL137C [P] NAM9 ribosomal protein, mitochondrial | | |
| <u> </u> | YNL137C | [P] NAM9 ribosomal protein, mitochondrial |

| VCD 21 IVI | [D] DDGGA 400 11 |
|-------------|---|
| YGR214W | [P] RPS0A 40S ribosomal protein p40 homolog A |
| YDR347W | [P] MRP1 ribosomal protein of the small subunit, mitochondrial |
| YNL306W | [P] MRPS18 ribosomal protein of the small subunit, mitochondrial |
| YOL120C | [P] RPL18A 60S large subunit ribosomal protein S18.e |
| YNL301C | [P] RPL18B 60S large subunit ribosomal protein L18.e |
| YGR084C | [P] MRP13 ribosomal protein of the small subunit, mitochondrial |
| YHL004W | [P] MRP4 ribosomal protein of the small subunit, mitochondrial |
| YPR187W | [T] RPO26 DNA-directed RNA polymerase I, II, III 18 KD subunit |
| YOR210W | [T] RPB10 DNA-directed polymerase I, II, III 8.3 subunit |
| YIL093C | [U] RSM25 weak similarity to S.pombe hypothetical protein SPBC16A3 |
| YKL155C | [U] RSM22 similarity to S. pombe SPAC1420.04c putative cytochrome c oxidase assembly |
| | protein |
| YJR008W | [U] YJR008w similarity to S.pombe hypothetical protein |
| YGL129C | [U] RSM23 similarity to S.pombe hypothetical protein SPBC29A3.15C - putative |
| | mitochondrial function |
| YDR036C | [U] YDR036c similarity to enoyl CoA hydratase |
| Q-clique 20 | Function Annotation |
| YLR244C | [F] MAP1 methionine aminopeptidase, isoform 1 |
| YBL091C | [F] MAP2 methionine aminopeptidase, isoform 2 |
| YDR226W | [M] ADK1 adenylate kinase, cytosolic |
| YJL063C | [P] MRPL8 ribosomal protein L17, mitochondrial |
| YGR118W | [P] RPS23A 40S small subunit ribosomal protein S23.e |
| YGL135W | [P] RPL1B 60S large subunit ribosomal protein |
| YEL054C | [P] RPL12A 60S large subunit ribosomal protein L12.e |
| YOR335C | [P] ALA1 alanyl-tRNA synthetase, cytosolic |
| YDL202W | [P] MRPL11 ribosomal protein of the large subunit, mitochondrial |
| YGL068W | [P] YGL068w strong similarity to Cricetus mitochrondial ribosomal L12 protein |
| YPL220W | [P] RPL1A ribosomal protein |
| YPR132W | [P] RPS23B 40S small subunit ribosomal protein S23.e |
| YPL183W-A | [P] YPL183w-a strong similarity to mitochondrial and bacterial ribosomal L36 proteins |
| YGL030W | [P] RPL30 60S large subunit ribosomal protein L30.e |
| YDR418W | [P] RPL12B 60S large subunit ribosomal protein L12.e |
| YHL015W | [P] RPS20 ribosomal protein |
| YLR340W | [P] RPP0 acidic ribosomal protein L10.e |
| YBL038W | [P] MRPL16 ribosomal protein of the large subunit, mitochondrial |
| YLR075W | [P] RPL10 60S large subunit ribosomal protein |
| YNL185C | [P] MRPL19 ribosomal protein of the large subunit, mitochondrial |
| YJR123W | [P] RPS5 ribosomal protein S5.e |
| YML009C | [P] MRPL39 60S ribosomal protein, mitochondrial |
| YMR260C | [P] TIF11 translation initiation factor eIF1a |
| YNR036C | [P] YNR036c strong similarity to ribosomal protein S12 |
| YDR116C | [P] YDR116c similarity to bacterial ribosomal L1 proteins |
| YML010W | [T] SPT5 transcription elongation protein |
| YBR154C | [T] RPB5 DNA-directed RNA polymerase I, II, III 25 KD subunit |
| YOR151C | [T] RPB2 DNA-directed RNA polymerase II, 140 kDa chain |
| YOR341W | [T] RPA190 DNA-directed RNA polymerase I, 190 KD alpha subunit |
| YPR010C | [T] RPA135 DNA-directed RNA polymerase I, 135 KD subunit |
| YDL140C | [T] RPO21 DNA-directed RNA polymerase II, 215 KD subunit |
| YKL009W | [T] MRT4 mRNA turnover 4 |
| YOR207C | [T] RET1 DNA-directed RNA polymerase III, 130 KD subunit |
| YOR116C | [T] RPO31 DNA-directed RNA polymerase III, 160 KD subunit |
| YDR101C | [U] YDR101c weak similarity to proliferation-associated protein |
| Q-clique 21 | Function Annotation |
| YLR153C | [E] ACS2 acetyl-coenzyme A synthetase |
| YER061C | [E] CEM1 beta-keto-acyl-ACP synthase, mitochondrial |

| VALO54C | |
|--------------------|--|
| YAL054C | [E] ACS1 acetyl-CoA synthetase |
| YKL182W | [M] FAS1 fatty-acyl-CoA synthase, beta chain |
| YKL192C | [M] ACP1 mitochonrial acyl-carrier protein |
| YPL231W | [M] FAS2 fatty-acyl-CoA synthase, alpha chain |
| YBR041W | [M] FAT1 very long-chain fatty acyl-CoA synthetase |
| YBR222C | [M] FAT2 AMP-binding protein, peroxisomal |
| YKR009C | [M] FOX2 hydratase-dehydrogenase-epimerase, peroxisomal |
| YNR016C | [M] ACC1 acetyl-CoA carboxylase |
| YBR208C | [M] DUR1,2 urea amidolyase |
| YNL137C | [P] NAM9 ribosomal protein, mitochondrial |
| YDR041W | [P] RSM10 component of the mitochondrial ribosomal small subunit |
| YNL306W | [P] MRPS18 ribosomal protein of the small subunit, mitochondrial |
| YDR347W | [P] MRP1 ribosomal protein of the small subunit, mitochondrial |
| YGR084C | [P] MRP13 ribosomal protein of the small subunit, mitochondrial |
| YPL118W | [P] MRP51 mitochondrial ribosomal protein of the small subunit |
| YJR113C | [P] RSM7 similarity to bacterial, chloroplast and mitochondrial ribosomal protein S7 |
| YDR337W | [P] MRPS28 ribosomal protein of the small subunit, mitochondrial |
| YIL093C | [U] RSM25 weak similarity to S.pombe hypothetical protein SPBC16A3 |
| YOR093C | [U] YOR093c similarity to S.pombe hypothetical protein SPAC22F3.04 |
| YKL155C | [U] RSM22 similarity to S. pombe SPAC1420.04c putative cytochrome c oxidase assembly |
| VDD026G | protein |
| YDR036C | [U] YDR036c similarity to enoyl CoA hydratase |
| YGL129C | [U] RSM23 similarity to S.pombe hypothetical protein SPBC29A3.15C - putative |
| 0 1 2 22 | mitochondrial function |
| Q-clique 22 | Function Annotation |
| YLR006C | [A] SSK1 two-component signal transducer |
| YDL235C | [A] YPD1 phosphorelay intermediate between SLN1P and SSK1P |
| YHR206W | [B] SKN7 transcription factor with similarity to HSF1P |
| YIL147C | [C] SLN1 two-component signal transducer |
| YFL033C YDR076W | [C] RIM15 protein kinase involved in expression of meiotic genes |
| | [D] RAD55 DNA repair protein |
| Q0250 Q0275 | [E] COX2 cytochrome-c oxidase subunit II [E] COX3 cytochrome-c oxidase chain III |
| Q0273 Q0045 | [E] COX3 cytochrome-c oxidase chain III [E] COX1 cytochrome-c oxidase subunit I |
| YGR112W | [E] SHY1 SURF homologue protein |
| YDR292C | [F] SRP101 signal recognition particle receptor, alpha chain |
| YDR127W | [G] ARO1 arom pentafunctional enzyme |
| YIL042C | [G] YIL042c similarity to rat branched-chain alpha-ketoacid dehydrogenase kinase |
| YKL104C | [M] GFA1 glucosaminefructose-6-phosphate transaminase |
| YNL123W | [U] YNL123w weak similarity to C.jejuni serine protease |
| YGL059W | [U] YGL059w similarity to rat branched-chain alpha-ketoacid dehydrogenase kinase |
| Q-clique 23 | Function Annotation |
| YNL306W | [P] MRPS18 ribosomal protein of the small subunit, mitochondrial |
| YJR113C | [P] RSM7 similarity to bacterial, chloroplast and mitochondrial ribosomal protein S7 |
| YDR347W | [P] MRP1 ribosomal protein of the small subunit, mitochondrial |
| YGR084C | [P] MRP13 ribosomal protein of the small subunit, mitochondrial |
| YDR041W | [P] RSM10 component of the mitochondrial ribosomal small subunit |
| YBR146W | [P] MRPS9 ribosomal protein S9 precursor, mitochondrial |
| YPL118W | [P] MRP51 mitochondrial ribosomal protein of the small subunit |
| YDR337W | [P] MRPS28 ribosomal protein of the small subunit, mitochondrial |
| YNL137C | [P] NAM9 ribosomal protein, mitochondrial |
| YGL129C | [U] RSM23 similarity to S.pombe hypothetical protein SPBC29A3.15C - putative |
| TGL127C | mitochondrial function |
| YIL093C | [U] RSM25 weak similarity to S.pombe hypothetical protein SPBC16A3 |
| YDR036C | [U] YDR036c similarity to enoyl CoA hydratase |
| | L-1 |

| YKL155C | [U] RSM22 similarity to S. pombe SPAC1420.04c putative cytochrome c oxidase assembly |
|-----------------------------|--|
| | protein |
| Q-clique 24 | Function Annotation |
| YMR208W | [M] ERG12 mevalonate kinase |
| YDL083C | [P] RPS16B ribosomal protein S16.e |
| YMR143W | [P] RPS16A ribosomal protein S16.e |
| YLR048W | [P] RPS0B 40S ribosomal protein p40 homolog B |
| YOR150W | [P] MRPL23 ribosomal protein of the large subunit, mitochondrial |
| YNL069C | [P] RPL16B 60S large subunit ribosomal protein |
| YNL301C | [P] RPL18B 60S large subunit ribosomal protein L18.e |
| YOL120C | [P] RPL18A 60S large subunit ribosomal protein S18.e |
| YIL133C | [P] RPL16A 60S large subunit ribosomal protein |
| YGR214W | [P] RPS0A 40S ribosomal protein p40 homolog A |
| YKL144C | [T] RPC25 DNA-directed RNA polymerase III, 25 KD subunit |
| YPR190C | [T] RPC82 DNA-directed RNA polymerase III, 82 KD subunit |
| YPR187W | [T] RPO26 DNA-directed RNA polymerase I, II, III 18 KD subunit |
| YDL150W | [T] RPC53 DNA-directed RNA polymerase III, 47 KD subunit |
| | [T] RPA135 DNA-directed RNA polymerase II, 135 KD subunit |
| YPR010C YNL113W | [T] RPC19 DNA-directed RNA polymerase I, III 16 KD subunit |
| | |
| YNL248C | [T] RPA49 DNA-directed RNA polymerase A (I) chain, 46 kDa |
| YKR025W | [T] RPC37 Pol III transcription |
| YPR110C | [T] RPC40 DNA-directed RNA polymerase I, III 40 KD subunit |
| YBR154C | [T] RPB5 DNA-directed RNA polymerase I, II, III 25 KD subunit |
| YNL151C | [T] RPC31 DNA-directed RNA polymerase III, 31 KD subunit |
| YNR003C | [T] RPC34 DNA-directed RNA polymerase III, 34 KD subunit |
| YOR116C | [T] RPO31 DNA-directed RNA polymerase III, 160 KD subunit |
| YOR207C | [T] RET1 DNA-directed RNA polymerase III, 130 KD subunit |
| YOR224C | [T] RPB8 DNA-directed RNA polymerase I, II, III 16 KD subunit |
| YOR210W | [T] RPB10 DNA-directed polymerase I, II, III 8.3 subunit |
| YJR008W | [U] YJR008w similarity to S.pombe hypothetical protein |
| Q-clique 25 | Function Annotation |
| YLR006C | [A] SSK1 two-component signal transducer |
| YHR206W | [B] SKN7 transcription factor with similarity to HSF1P |
| YIL147C | [C] SLN1 two-component signal transducer |
| YFL033C | [C] RIM15 protein kinase involved in expression of meiotic genes |
| YML054C | [E] CYB2 lactate dehydrogenase cytochrome b2 |
| YGR112W | [E] SHY1 SURF homologue protein |
| Q0275 | [E] COX3 cytochrome-c oxidase chain III |
| Q0045 | [E] COX1 cytochrome-c oxidase subunit I |
| Q0250 | [E] COX2 cytochrome-c oxidase subunit II |
| YDR292C | [F] SRP101 signal recognition particle receptor, alpha chain |
| YIL042C | [G] YIL042c similarity to rat branched-chain alpha-ketoacid dehydrogenase kinase |
| YER069W | [G] ARG5,6 acetylglutamate kinase and acetylglutamyl-phosphate reductase |
| YDR127W | [G] ARO1 arom pentafunctional enzyme |
| YGL059W | [U] YGL059w similarity to rat branched-chain alpha-ketoacid dehydrogenase kinase |
| Q-clique 26 | Function Annotation |
| YLR447C | [A] VMA6 H+-ATPase V0 domain 36 KD subunit, vacuolar |
| YGR020C | [A] VMA7 H+-ATPase V1 domain 14 kDa subunit, vacuolar |
| YHR026W | [A] PPA1 H+-ATPase 23 KD subunit, vacuolar |
| 1 | |
| YMR054W | [A] STV1 H+-ATPase V0 domain 102 KD subunit, not vacuolar |
| YEL051W | [A] STV1 H+-ATPase V0 domain 102 KD subunit, not vacuolar [A] VMA8 H+-ATPsynthase V1 domain 32 KD subunit, vacuolar |
| | [A] STV1 H+-ATPase V0 domain 102 KD subunit, not vacuolar |
| YEL051W YDL227C Q0130 | [A] STV1 H+-ATPase V0 domain 102 KD subunit, not vacuolar [A] VMA8 H+-ATPsynthase V1 domain 32 KD subunit, vacuolar [C] HO homothallic switching endonuclease [E] OLI1 F1F0-ATPase complex, F0 subunit 9 |
| YEL051W YDL227C | [A] STV1 H+-ATPase V0 domain 102 KD subunit, not vacuolar [A] VMA8 H+-ATPsynthase V1 domain 32 KD subunit, vacuolar [C] HO homothallic switching endonuclease |

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| YOR332W | [O] VMA4 H+-ATPase V1 domain 27 KD subunit, vacuolar |
| YPL234C | [O] TFP3 H+-ATPase V0 domain 17 KD subunit, vacuolar |
| YOR270C | [O] VPH1 H+-ATPase V0 domain 95K subunit, vacuolar |
| YDL185W | [O] TFP1 H+-ATPase V1 domain 69 KD catalytic subunit, vacuolar |
| YPR010C | [T] RPA135 DNA-directed RNA polymerase I, 135 KD subunit |
| YDL150W | [T] RPC53 DNA-directed RNA polymerase III, 47 KD subunit |
| YNL113W | [T] RPC19 DNA-directed RNA polymerase I,III 16 KD subunit |
| YKR025W | [T] RPC37 Pol III transcription |
| YBR154C | [T] RPB5 DNA-directed RNA polymerase I, II, III 25 KD subunit |
| YNL248C | [T] RPA49 DNA-directed RNA polymerase A (I) chain, 46 kDa |
| YNR003C | [T] RPC34 DNA-directed RNA polymerase III, 34 KD subunit |
| YOR341W | [T] RPA190 DNA-directed RNA polymerase I, 190 KD alpha subunit |
| YNL151C | [T] RPC31 DNA-directed RNA polymerase III, 31 KD subunit |
| YOR116C | [T] RPO31 DNA-directed RNA polymerase III, 160 KD subunit |
| YOR207C | [T] RET1 DNA-directed RNA polymerase III, 130 KD subunit |
| YKL144C | [T] RPC25 DNA-directed RNA polymerase III, 25 KD subunit |
| YOR224C | [T] RPB8 DNA-directed RNA polymerase I, II, III 16 KD subunit |
| YPR187W | [T] RPO26 DNA-directed RNA polymerase I, II, III 18 KD subunit |
| YPR190C | [T] RPC82 DNA-directed RNA polymerase III, 82 KD subunit |
| Q-clique 27 | Function Annotation |
| YNL189W | [O] SRP1 karyopherin-alpha or importin |
| YDR432W | [O] NPL3 nucleolar protein |
| YLR347C | [O] KAP95 karyopherin-beta |
| YGR162W | [P] TIF4631 mRNA cap-binding protein (eIF4F), 150K subunit |
| YGL049C | [P] TIF4632 mRNA cap-binding protein (eIF4F), 130K subunit |
| YLR298C | [T] YHC1 associated with the U1 snRNP complex |
| YGR074W | [T] SMD1 snRNA-associated protein |
| YML046W | [T] PRP39 pre-mRNA splicing factor [T] PRP40 splicing factor |
| YKL012W YPL178W | [T] CBC2 small subunit of the nuclear cap-binding protein complex CBC |
| YDL087C | [T] LUC7 yeast U1 snRNP protein with a role in 5' splice site recognition |
| YLR275W | [T] SMD2 U1 snRNP protein of the Sm class |
| YLR147C | [T] SMD3 spliceosomal snRNA-associated Sm core protein required for pre-mRNA |
| TERTITE | splicing |
| YGR013W | [T] SNU71 associated with U1 snRNP, no counterpart in mammalian U1 snRNP |
| YDR235W | [T] PRP42 U1 snRNP associated protein, required for pre-mRNA splicing |
| YER029C | [T] SMB1 associated with U1 snRNP as part of the Sm-core that is common to all |
| | spliceosomal snRNPs |
| YHR086W | [T] NAM8 meiotic recombination protein |
| YMR125W | [T] STO1 large subunit of the nuclear cap-binding protein complex CBC |
| YIL061C | [T] SNP1 U1 small nuclear ribonucleoprotein |
| YDR240C | [T] SNU56 U1 snRNA protein, no counterpart in mammalian snRNP |
| YBR119W | [T] MUD1 U1 snRNP-specific A protein |
| Q-clique 28 | Function Annotation |
| YLR117C | [D] CLF1 strong similarity to Drosophila putative cell cycle control protein crn |
| YDR364C | [D] CDC40 cell division control protein |
| YMR213W | [D] CEF1 required during G2/M transition |
| YML049C | [O] RSE1 involved in RNA splicing and ER to Golgi transport |
| YKL173W | [P] SNU114 U5 snRNP-specific protein |
| YGL128C | [R] YGL128c weak similarity to dnaJ proteins |
| YDL030W | [T] PRP9 pre-mRNA splicing factor (snRNA-associated protein) |
| YPR101W | [T] SNT309 splicing factor |
| YGR091W | [T] PRP31 pre-mRNA splicing protein |
| YPR178W | T] PRP4 U4/U6 snRNP 52 KD protein |
| YLL036C | [T] PRP19 non-snRNP sliceosome component required for DNA repair |

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| YJL203W | [T] PRP21 pre-mRNA splicing factor |
| YMR240C | [T] CUS1 U2 snRNP protein |
| YBR055C | [T] PRP6 snRNP(U4/U6)-associated splicing factor |
| YPL213W | [T] LEA1 U2 A'snRNP protein |
| YDR416W | [T] SYF1 synthetic lethal with CDC40 |
| YMR288W | [T] HSH155 component of a multiprotein splicing factor |
| YGL120C | [T] PRP43 involved in spliceosome disassembly |
| YAL032C | [T] PRP45 pre-mRNA splicing factor |
| YGR278W | [U] YGR278w similarity to C.elegans LET-858 |
| YLR424W | [U] YLR424w weak similarity to STU1P |
| YPL151C | [U] PRP46 strong similarity to A.thaliana PRL1 and PRL2 proteins |
| YDL209C | [U] YDL209c similarity to hypothetical S. pombe protein |
| Q-clique 29 | Function Annotation |
| YJR113C | [P] RSM7 similarity to bacterial, chloroplast and mitochondrial ribosomal protein S7 |
| YGL030W | [P] RPL30 60S large subunit ribosomal protein L30.e |
| YNL113W | [T] RPC19 DNA-directed RNA polymerase I,III 16 KD subunit |
| YKR025W | [T] RPC37 Pol III transcription |
| YBR154C | [T] RPB5 DNA-directed RNA polymerase I, II, III 25 KD subunit |
| YJR063W | [T] RPA12 DNA-directed RNA polymerase I, 13.7 KD subunit |
| YOR341W | [T] RPA190 DNA-directed RNA polymerase I, 190 KD alpha subunit |
| YNL248C | [T] RPA49 DNA-directed RNA polymerase A (I) chain, 46 kDa |
| YNR003C | [T] RPC34 DNA-directed RNA polymerase III, 34 KD subunit |
| YNL151C | [T] RPC31 DNA-directed RNA polymerase III, 31 KD subunit |
| YKL144C | [T] RPC25 DNA-directed RNA polymerase III, 25 KD subunit |
| YOR116C | [T] RPO31 DNA-directed RNA polymerase III, 160 KD subunit |
| YPR190C | [T] RPC82 DNA-directed RNA polymerase III, 82 KD subunit |
| YOR207C | [T] RET1 DNA-directed RNA polymerase III, 130 KD subunit |
| YOR224C | [T] RPB8 DNA-directed RNA polymerase I, II, III 16 KD subunit |
| | - · |
| YDL150W | [T] RPC53 DNA-directed RNA polymerase III, 47 KD subunit |
| YPR010C | [T] RPC53 DNA-directed RNA polymerase III, 47 KD subunit [T] RPA135 DNA-directed RNA polymerase I, 135 KD subunit |
| YPR010C Q-clique 30 | [T] RPC53 DNA-directed RNA polymerase III, 47 KD subunit [T] RPA135 DNA-directed RNA polymerase I, 135 KD subunit Function Annotation |
| YPR010C Q-clique 30 YEL051W | [T] RPC53 DNA-directed RNA polymerase III, 47 KD subunit [T] RPA135 DNA-directed RNA polymerase I, 135 KD subunit Function Annotation [A] VMA8 H+-ATPsynthase V1 domain 32 KD subunit, vacuolar |
| YPR010C Q-clique 30 YEL051W YHR026W | [T] RPC53 DNA-directed RNA polymerase III, 47 KD subunit [T] RPA135 DNA-directed RNA polymerase I, 135 KD subunit Function Annotation [A] VMA8 H+-ATPsynthase V1 domain 32 KD subunit, vacuolar [A] PPA1 H+-ATPase 23 KD subunit, vacuolar |
| YPR010C Q-clique 30 YEL051W YHR026W YGR020C | [T] RPC53 DNA-directed RNA polymerase III, 47 KD subunit [T] RPA135 DNA-directed RNA polymerase I, 135 KD subunit Function Annotation [A] VMA8 H+-ATPsynthase V1 domain 32 KD subunit, vacuolar [A] PPA1 H+-ATPase 23 KD subunit, vacuolar [A] VMA7 H+-ATPase V1 domain 14 kDa subunit, vacuolar |
| YPR010C Q-clique 30 YEL051W YHR026W YGR020C YLR447C | [T] RPC53 DNA-directed RNA polymerase III, 47 KD subunit [T] RPA135 DNA-directed RNA polymerase I, 135 KD subunit Function Annotation [A] VMA8 H+-ATPsynthase V1 domain 32 KD subunit, vacuolar [A] PPA1 H+-ATPase 23 KD subunit, vacuolar [A] VMA7 H+-ATPase V1 domain 14 kDa subunit, vacuolar [A] VMA6 H+-ATPase V0 domain 36 KD subunit, vacuolar |
| YPR010C Q-clique 30 YEL051W YHR026W YGR020C YLR447C Q0130 | [T] RPC53 DNA-directed RNA polymerase III, 47 KD subunit [T] RPA135 DNA-directed RNA polymerase I, 135 KD subunit Function Annotation [A] VMA8 H+-ATPsynthase V1 domain 32 KD subunit, vacuolar [A] PPA1 H+-ATPase 23 KD subunit, vacuolar [A] VMA7 H+-ATPase V1 domain 14 kDa subunit, vacuolar [A] VMA6 H+-ATPase V0 domain 36 KD subunit, vacuolar [E] OLI1 F1F0-ATPase complex, F0 subunit 9 |
| YPR010C Q-clique 30 YEL051W YHR026W YGR020C YLR447C Q0130 YJR121W | [T] RPC53 DNA-directed RNA polymerase III, 47 KD subunit [T] RPA135 DNA-directed RNA polymerase I, 135 KD subunit Function Annotation [A] VMA8 H+-ATPsynthase V1 domain 32 KD subunit, vacuolar [A] PPA1 H+-ATPase 23 KD subunit, vacuolar [A] VMA7 H+-ATPase V1 domain 14 kDa subunit, vacuolar [A] VMA6 H+-ATPase V0 domain 36 KD subunit, vacuolar [E] OLI1 F1F0-ATPase complex, F0 subunit 9 [E] ATP2 F1F0-ATPase complex, F1 beta subunit |
| YPR010C Q-clique 30 YEL051W YHR026W YGR020C YLR447C Q0130 YJR121W Q0085 | [T] RPC53 DNA-directed RNA polymerase III, 47 KD subunit [T] RPA135 DNA-directed RNA polymerase I, 135 KD subunit Function Annotation [A] VMA8 H+-ATPsynthase V1 domain 32 KD subunit, vacuolar [A] PPA1 H+-ATPase 23 KD subunit, vacuolar [A] VMA7 H+-ATPase V1 domain 14 kDa subunit, vacuolar [A] VMA6 H+-ATPase V0 domain 36 KD subunit, vacuolar [E] OLI1 F1F0-ATPase complex, F0 subunit 9 [E] ATP2 F1F0-ATPase complex, F1 beta subunit [E] ATP6 F1F0-ATPase complex, FO A subunit |
| YPR010C Q-clique 30 YEL051W YHR026W YGR020C YLR447C Q0130 YJR121W Q0085 YDR298C | [T] RPC53 DNA-directed RNA polymerase III, 47 KD subunit [T] RPA135 DNA-directed RNA polymerase I, 135 KD subunit Function Annotation [A] VMA8 H+-ATPsynthase V1 domain 32 KD subunit, vacuolar [A] PPA1 H+-ATPase 23 KD subunit, vacuolar [A] VMA7 H+-ATPase V1 domain 14 kDa subunit, vacuolar [A] VMA6 H+-ATPase V0 domain 36 KD subunit, vacuolar [E] OLI1 F1F0-ATPase complex, F0 subunit 9 [E] ATP2 F1F0-ATPase complex, F1 beta subunit [E] ATP6 F1F0-ATPase complex, FO A subunit [E] ATP5 F1F0-ATPase complex, OSCP subunit |
| YPR010C Q-clique 30 YEL051W YHR026W YGR020C YLR447C Q0130 YJR121W Q0085 YDR298C YBL099W | [T] RPC53 DNA-directed RNA polymerase III, 47 KD subunit [T] RPA135 DNA-directed RNA polymerase I, 135 KD subunit Function Annotation [A] VMA8 H+-ATPsynthase V1 domain 32 KD subunit, vacuolar [A] PPA1 H+-ATPase 23 KD subunit, vacuolar [A] VMA7 H+-ATPase V1 domain 14 kDa subunit, vacuolar [A] VMA6 H+-ATPase V0 domain 36 KD subunit, vacuolar [E] OLI1 F1F0-ATPase complex, F0 subunit 9 [E] ATP2 F1F0-ATPase complex, F1 beta subunit [E] ATP5 F1F0-ATPase complex, FO A subunit [E] ATP5 F1F0-ATPase complex, FO A subunit [E] ATP1 F1F0-ATPase complex, F1 alpha subunit |
| YPR010C Q-clique 30 YEL051W YHR026W YGR020C YLR447C Q0130 YJR121W Q0085 YDR298C YBL099W YDL004W | [T] RPC53 DNA-directed RNA polymerase III, 47 KD subunit [T] RPA135 DNA-directed RNA polymerase I, 135 KD subunit Function Annotation [A] VMA8 H+-ATPsynthase V1 domain 32 KD subunit, vacuolar [A] PPA1 H+-ATPase 23 KD subunit, vacuolar [A] VMA7 H+-ATPase V1 domain 14 kDa subunit, vacuolar [A] VMA6 H+-ATPase V0 domain 36 KD subunit, vacuolar [E] OLI1 F1F0-ATPase complex, F0 subunit 9 [E] ATP2 F1F0-ATPase complex, F1 beta subunit [E] ATP6 F1F0-ATPase complex, FO A subunit [E] ATP1 F1F0-ATPase complex, F1 alpha subunit [E] ATP1 F1F0-ATPase complex, F1 delta subunit |
| YPR010C Q-clique 30 YEL051W YHR026W YGR020C YLR447C Q0130 YJR121W Q0085 YDR298C YBL099W YDL004W YBR039W | [T] RPC53 DNA-directed RNA polymerase III, 47 KD subunit [T] RPA135 DNA-directed RNA polymerase I, 135 KD subunit Function Annotation [A] VMA8 H+-ATPsynthase V1 domain 32 KD subunit, vacuolar [A] PPA1 H+-ATPase 23 KD subunit, vacuolar [A] VMA7 H+-ATPase V1 domain 14 kDa subunit, vacuolar [A] VMA6 H+-ATPase V0 domain 36 KD subunit, vacuolar [E] OLI1 F1F0-ATPase complex, F0 subunit 9 [E] ATP2 F1F0-ATPase complex, F1 beta subunit [E] ATP6 F1F0-ATPase complex, FO A subunit [E] ATP5 F1F0-ATPase complex, F3 alpha subunit [E] ATP1 F1F0-ATPase complex, F1 delta subunit [E] ATP1 F1F0-ATPase complex, F1 delta subunit [E] ATP1 F1F0-ATPase complex, F1 gamma subunit |
| YPR010C Q-clique 30 YEL051W YHR026W YGR020C YLR447C Q0130 YJR121W Q0085 YDR298C YBL099W YDL004W YBR039W YBR127C | [T] RPC53 DNA-directed RNA polymerase III, 47 KD subunit [T] RPA135 DNA-directed RNA polymerase I, 135 KD subunit Function Annotation [A] VMA8 H+-ATPsynthase V1 domain 32 KD subunit, vacuolar [A] PPA1 H+-ATPase 23 KD subunit, vacuolar [A] VMA7 H+-ATPase V1 domain 14 kDa subunit, vacuolar [A] VMA6 H+-ATPase V0 domain 36 KD subunit, vacuolar [E] OLI1 F1F0-ATPase complex, F0 subunit 9 [E] ATP2 F1F0-ATPase complex, F1 beta subunit [E] ATP6 F1F0-ATPase complex, FO A subunit [E] ATP5 F1F0-ATPase complex, OSCP subunit [E] ATP1 F1F0-ATPase complex, F1 alpha subunit [E] ATP1 F1F0-ATPase complex, F1 delta subunit [E] ATP3 F1F0-ATPase complex, F1 gamma subunit [O] VMA2 H+-ATPase V1 domain 60 KD subunit, vacuolar |
| YPR010C Q-clique 30 YEL051W YHR026W YGR020C YLR447C Q0130 YJR121W Q0085 YDR298C YBL099W YDL004W YBR039W YBR127C YEL027W | [T] RPC53 DNA-directed RNA polymerase III, 47 KD subunit [T] RPA135 DNA-directed RNA polymerase I, 135 KD subunit Function Annotation [A] VMA8 H+-ATPsynthase V1 domain 32 KD subunit, vacuolar [A] PPA1 H+-ATPase 23 KD subunit, vacuolar [A] VMA7 H+-ATPase V1 domain 14 kDa subunit, vacuolar [A] VMA6 H+-ATPase V0 domain 36 KD subunit, vacuolar [E] OLI1 F1F0-ATPase complex, F0 subunit 9 [E] ATP2 F1F0-ATPase complex, F1 beta subunit [E] ATP6 F1F0-ATPase complex, FO A subunit [E] ATP5 F1F0-ATPase complex, OSCP subunit [E] ATP1 F1F0-ATPase complex, F1 alpha subunit [E] ATP1 F1F0-ATPase complex, F1 delta subunit [E] ATP3 F1F0-ATPase complex, F1 gamma subunit [O] VMA2 H+-ATPase V1 domain 60 KD subunit, vacuolar [O] CUP5 H+-ATPase V0 domain 17 KD subunit, vacuolar |
| YPR010C Q-clique 30 YEL051W YHR026W YGR020C YLR447C Q0130 YJR121W Q0085 YDR298C YBL099W YDL004W YBR039W YBR127C YEL027W YOR332W | [T] RPC53 DNA-directed RNA polymerase III, 47 KD subunit [T] RPA135 DNA-directed RNA polymerase I, 135 KD subunit Function Annotation [A] VMA8 H+-ATPsynthase V1 domain 32 KD subunit, vacuolar [A] PPA1 H+-ATPase 23 KD subunit, vacuolar [A] VMA7 H+-ATPase V1 domain 14 kDa subunit, vacuolar [A] VMA6 H+-ATPase V0 domain 36 KD subunit, vacuolar [E] OLI1 F1F0-ATPase complex, F0 subunit 9 [E] ATP2 F1F0-ATPase complex, F1 beta subunit [E] ATP6 F1F0-ATPase complex, FO A subunit [E] ATP5 F1F0-ATPase complex, FO A subunit [E] ATP1 F1F0-ATPase complex, F1 alpha subunit [E] ATP16 F1F0-ATPase complex, F1 delta subunit [E] ATP3 F1F0-ATPase complex, F1 gamma subunit [O] VMA2 H+-ATPase V1 domain 60 KD subunit, vacuolar [O] CUP5 H+-ATPase V0 domain 17 KD subunit, vacuolar |
| YPR010C Q-clique 30 YEL051W YHR026W YGR020C YLR447C Q0130 YJR121W Q0085 YDR298C YBL099W YDL004W YBR039W YBR127C YEL027W YOR332W YPL234C | [T] RPC53 DNA-directed RNA polymerase III, 47 KD subunit [T] RPA135 DNA-directed RNA polymerase I, 135 KD subunit Function Annotation [A] VMA8 H+-ATPsynthase V1 domain 32 KD subunit, vacuolar [A] PPA1 H+-ATPase 23 KD subunit, vacuolar [A] VMA7 H+-ATPase V1 domain 14 kDa subunit, vacuolar [A] VMA6 H+-ATPase V0 domain 36 KD subunit, vacuolar [E] OLI1 F1F0-ATPase complex, F0 subunit 9 [E] ATP2 F1F0-ATPase complex, F1 beta subunit [E] ATP6 F1F0-ATPase complex, FO A subunit [E] ATP5 F1F0-ATPase complex, OSCP subunit [E] ATP1 F1F0-ATPase complex, F1 alpha subunit [E] ATP1 F1F0-ATPase complex, F1 delta subunit [E] ATP3 F1F0-ATPase complex, F1 gamma subunit [O] VMA2 H+-ATPase V1 domain 60 KD subunit, vacuolar [O] CUP5 H+-ATPase V1 domain 27 KD subunit, vacuolar [O] TFP3 H+-ATPase V1 domain 17 KD subunit, vacuolar |
| YPR010C Q-clique 30 YEL051W YHR026W YGR020C YLR447C Q0130 YJR121W Q0085 YDR298C YBL099W YDL004W YBR039W YBR127C YEL027W YOR332W YPL234C YDL185W | [T] RPC53 DNA-directed RNA polymerase III, 47 KD subunit [T] RPA135 DNA-directed RNA polymerase I, 135 KD subunit Function Annotation [A] VMA8 H+-ATPsynthase V1 domain 32 KD subunit, vacuolar [A] PPA1 H+-ATPase 23 KD subunit, vacuolar [A] VMA7 H+-ATPase V1 domain 14 kDa subunit, vacuolar [A] VMA6 H+-ATPase V0 domain 36 KD subunit, vacuolar [E] OLI1 F1F0-ATPase complex, F0 subunit 9 [E] ATP2 F1F0-ATPase complex, F1 beta subunit [E] ATP6 F1F0-ATPase complex, FO A subunit [E] ATP5 F1F0-ATPase complex, FS abbunit [E] ATP1 F1F0-ATPase complex, F1 alpha subunit [E] ATP1 F1F0-ATPase complex, F1 delta subunit [E] ATP3 F1F0-ATPase complex, F1 gamma subunit [O] VMA2 H+-ATPase V1 domain 60 KD subunit, vacuolar [O] CUP5 H+-ATPase V1 domain 17 KD subunit, vacuolar [O] TFP3 H+-ATPase V1 domain 17 KD subunit, vacuolar [O] TFP1 H+-ATPase V1 domain 69 KD catalytic subunit, vacuolar |
| YPR010C Q-clique 30 YEL051W YHR026W YGR020C YLR447C Q0130 YJR121W Q0085 YDR298C YBL099W YDL004W YBR039W YBR127C YEL027W YOR332W YPL234C YDL185W YGL236C | [T] RPC53 DNA-directed RNA polymerase III, 47 KD subunit [T] RPA135 DNA-directed RNA polymerase I, 135 KD subunit Function Annotation [A] VMA8 H+-ATPsynthase V1 domain 32 KD subunit, vacuolar [A] PPA1 H+-ATPase 23 KD subunit, vacuolar [A] VMA7 H+-ATPase V1 domain 14 kDa subunit, vacuolar [A] VMA6 H+-ATPase V0 domain 36 KD subunit, vacuolar [E] OLI1 F1F0-ATPase complex, F0 subunit 9 [E] ATP2 F1F0-ATPase complex, F1 beta subunit [E] ATP6 F1F0-ATPase complex, FO A subunit [E] ATP5 F1F0-ATPase complex, F0 A subunit [E] ATP1 F1F0-ATPase complex, F1 alpha subunit [E] ATP1 F1F0-ATPase complex, F1 delta subunit [E] ATP3 F1F0-ATPase complex, F1 gamma subunit [O] VMA2 H+-ATPase V1 domain 60 KD subunit, vacuolar [O] CUP5 H+-ATPase V0 domain 17 KD subunit, vacuolar [O] TFP3 H+-ATPase V1 domain 69 KD catalytic subunit, vacuolar [O] TFP1 H+-ATPase V1 domain 69 KD catalytic subunit, vacuolar [P] MTO1 strong similarity to gidA E.coli protein |
| YPR010C Q-clique 30 YEL051W YHR026W YGR020C YLR447C Q0130 YJR121W Q0085 YDR298C YBL099W YDL004W YBR039W YBR127C YEL027W YOR332W YPL234C YDL185W YGL236C YLR289W | [T] RPC53 DNA-directed RNA polymerase III, 47 KD subunit [T] RPA135 DNA-directed RNA polymerase I, 135 KD subunit Function Annotation [A] VMA8 H+-ATPsynthase V1 domain 32 KD subunit, vacuolar [A] PPA1 H+-ATPase 23 KD subunit, vacuolar [A] VMA7 H+-ATPase V1 domain 14 kDa subunit, vacuolar [A] VMA6 H+-ATPase V0 domain 36 KD subunit, vacuolar [E] OLI1 F1F0-ATPase complex, F0 subunit 9 [E] ATP2 F1F0-ATPase complex, F1 beta subunit [E] ATP6 F1F0-ATPase complex, F0 A subunit [E] ATP5 F1F0-ATPase complex, F1 alpha subunit [E] ATP1 F1F0-ATPase complex, F1 alpha subunit [E] ATP16 F1F0-ATPase complex, F1 delta subunit [E] ATP3 F1F0-ATPase complex, F1 gamma subunit [O] VMA2 H+-ATPase V1 domain 60 KD subunit, vacuolar [O] CUP5 H+-ATPase V0 domain 17 KD subunit, vacuolar [O] TFP3 H+-ATPase V1 domain 69 KD catalytic subunit, vacuolar [O] TFP1 H+-ATPase V1 domain 69 KD catalytic subunit, vacuolar [P] MTO1 strong similarity to gidA E.coli protein [P] GUF1 strong similarity to E. coli elongation factor-type GTP-binding protein lepa |
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| YPR010C Q-clique 30 YEL051W YHR026W YGR020C YLR447C Q0130 YJR121W Q0085 YDR298C YBL099W YDL004W YBR039W YBL127C YEL027W YOR332W YPL234C YDL185W YGL236C YLR289W Q-clique 31 YMR118C | [T] RPC53 DNA-directed RNA polymerase III, 47 KD subunit [T] RPA135 DNA-directed RNA polymerase I, 135 KD subunit Function Annotation [A] VMA8 H+-ATPsynthase V1 domain 32 KD subunit, vacuolar [A] PPA1 H+-ATPase 23 KD subunit, vacuolar [A] VMA7 H+-ATPase V1 domain 14 kDa subunit, vacuolar [A] VMA6 H+-ATPase V0 domain 36 KD subunit, vacuolar [E] OLI1 F1F0-ATPase complex, F0 subunit 9 [E] ATP2 F1F0-ATPase complex, F1 beta subunit [E] ATP6 F1F0-ATPase complex, F0 A subunit [E] ATP5 F1F0-ATPase complex, F1 alpha subunit [E] ATP1 F1F0-ATPase complex, F1 alpha subunit [E] ATP1 F1F0-ATPase complex, F1 delta subunit [E] ATP3 F1F0-ATPase complex, F1 gamma subunit [O] VMA2 H+-ATPase V1 domain 60 KD subunit, vacuolar [O] CUP5 H+-ATPase V1 domain 17 KD subunit, vacuolar [O] TFP3 H+-ATPase V1 domain 27 KD subunit, vacuolar [O] TFP1 H+-ATPase V1 domain 69 KD catalytic subunit, vacuolar [P] MTO1 strong similarity to gidA E.coli protein [P] GUF1 strong similarity to E. coli elongation factor-type GTP-binding protein lepa Function Annotation [E] YMR118c strong similarity to succinate dehydrogenase |
| YPR010C Q-clique 30 YEL051W YHR026W YGR020C YLR447C Q0130 YJR121W Q0085 YDR298C YBL099W YDL004W YBR039W YBR127C YEL027W YOR332W YPL234C YDL185W YGL236C YLR289W Q-clique 31 YMR118C YLL041C | [T] RPC53 DNA-directed RNA polymerase III, 47 KD subunit [T] RPA135 DNA-directed RNA polymerase I, 135 KD subunit Function Annotation [A] VMA8 H+-ATPsynthase V1 domain 32 KD subunit, vacuolar [A] PPA1 H+-ATPase 23 KD subunit, vacuolar [A] VMA7 H+-ATPase V1 domain 14 kDa subunit, vacuolar [A] VMA6 H+-ATPase V0 domain 36 KD subunit, vacuolar [E] OL11 F1F0-ATPase complex, F0 subunit 9 [E] ATP2 F1F0-ATPase complex, F1 beta subunit [E] ATP6 F1F0-ATPase complex, F0 A subunit [E] ATP5 F1F0-ATPase complex, F1 alpha subunit [E] ATP1 F1F0-ATPase complex, F1 alpha subunit [E] ATP1 F1F0-ATPase complex, F1 gamma subunit [E] ATP3 F1F0-ATPase complex, F1 gamma subunit [O] VMA2 H+-ATPase V1 domain 60 KD subunit, vacuolar [O] CUP5 H+-ATPase V1 domain 27 KD subunit, vacuolar [O] TFP3 H+-ATPase V1 domain 27 KD subunit, vacuolar [O] TFP3 H+-ATPase V1 domain 69 KD catalytic subunit, vacuolar [P] MTO1 strong similarity to gidA E.coli protein [P] GUF1 strong similarity to E. coli elongation factor-type GTP-binding protein lepa Function Annotation [E] YMR118c strong similarity to succinate dehydrogenase [E] SDH2 succinate dehydrogenase iron-sulfur protein subunit |
| YPR010C Q-clique 30 YEL051W YHR026W YGR020C YLR447C Q0130 YJR121W Q0085 YDR298C YBL099W YDL004W YBR039W YBR127C YEL027W YOR332W YPL234C YDL185W YGL236C YLR289W Q-clique 31 YMR118C YLL041C YDR148C | [T] RPC53 DNA-directed RNA polymerase III, 47 KD subunit [T] RPA135 DNA-directed RNA polymerase I, 135 KD subunit Function Annotation [A] VMA8 H+-ATPsynthase V1 domain 32 KD subunit, vacuolar [A] PPA1 H+-ATPase 23 KD subunit, vacuolar [A] VMA7 H+-ATPase V1 domain 14 kDa subunit, vacuolar [A] VMA6 H+-ATPase V0 domain 36 KD subunit, vacuolar [E] OL11 F1F0-ATPase complex, F0 subunit 9 [E] ATP2 F1F0-ATPase complex, F1 beta subunit [E] ATP5 F1F0-ATPase complex, F0 A subunit [E] ATP6 F1F0-ATPase complex, F0 A subunit [E] ATP1 F1F0-ATPase complex, F1 delta subunit [E] ATP1 F1F0-ATPase complex, F1 delta subunit [E] ATP3 F1F0-ATPase complex, F1 gamma subunit [O] VMA2 H+-ATPase V1 domain 60 KD subunit, vacuolar [O] CUP5 H+-ATPase V1 domain 17 KD subunit, vacuolar [O] TFP3 H+-ATPase V1 domain 27 KD subunit, vacuolar [O] TFP1 H+-ATPase V1 domain 69 KD catalytic subunit, vacuolar [P] MTO1 strong similarity to gidA E.coli protein [P] GUF1 strong similarity to E. coli elongation factor-type GTP-binding protein lepa Function Annotation [E] YMR118c strong similarity to succinate dehydrogenase [E] SDH2 succinate dehydrogenase iron-sulfur protein subunit [E] KGD2 2-oxoglutarate dehydrogenase complex E2 component |
| YPR010C Q-clique 30 YEL051W YHR026W YGR020C YLR447C Q0130 YJR121W Q0085 YDR298C YBL099W YDL004W YBR039W YBR127C YEL027W YOR332W YPL234C YDL185W YGL236C YLR289W Q-clique 31 YMR118C YLL041C | [T] RPC53 DNA-directed RNA polymerase III, 47 KD subunit [T] RPA135 DNA-directed RNA polymerase I, 135 KD subunit Function Annotation [A] VMA8 H+-ATPsynthase V1 domain 32 KD subunit, vacuolar [A] PPA1 H+-ATPase 23 KD subunit, vacuolar [A] VMA7 H+-ATPase V1 domain 14 kDa subunit, vacuolar [A] VMA6 H+-ATPase V0 domain 36 KD subunit, vacuolar [E] OL11 F1F0-ATPase complex, F0 subunit 9 [E] ATP2 F1F0-ATPase complex, F1 beta subunit [E] ATP6 F1F0-ATPase complex, F0 A subunit [E] ATP5 F1F0-ATPase complex, F1 alpha subunit [E] ATP1 F1F0-ATPase complex, F1 alpha subunit [E] ATP1 F1F0-ATPase complex, F1 gamma subunit [E] ATP3 F1F0-ATPase complex, F1 gamma subunit [O] VMA2 H+-ATPase V1 domain 60 KD subunit, vacuolar [O] CUP5 H+-ATPase V1 domain 27 KD subunit, vacuolar [O] TFP3 H+-ATPase V1 domain 27 KD subunit, vacuolar [O] TFP3 H+-ATPase V1 domain 69 KD catalytic subunit, vacuolar [P] MTO1 strong similarity to gidA E.coli protein [P] GUF1 strong similarity to E. coli elongation factor-type GTP-binding protein lepa Function Annotation [E] YMR118c strong similarity to succinate dehydrogenase [E] SDH2 succinate dehydrogenase iron-sulfur protein subunit |

| YBR221C | [E] PDB1 pyruvate dehydrogenase (lipoamide) beta chain precursor |
|--|--|
| YIL125W | [E] KGD1 2-oxoglutarate dehydrogenase complex E1 component |
| YNL071W | [E] LAT1 dihydrolipoamide S-acetyltransferase |
| YGR244C | [E] LSC2 succinate-CoA ligase beta subunit |
| YKL141W | [E] SDH3 cytochrome b560 subunit of respiratory complex II |
| YGR193C | [E] PDX1 pyruvate dehydrogenase complex protein X |
| YOR375C | [G] GDH1 glutamate dehydrogenase (NADP+) |
| YFL018C | [G] LPD1 dihydrolipoamide dehydrogenase precursor |
| YAL062W | [G] GDH3 NADP-glutamate dehydrogenase |
| YML022W | [M] APT1 adenine phosphoribosyltransferase |
| YOR196C | [M] LIP5 lipoic acid synthase |
| YDR441C | [M] APT2 adenine phosphoribosyltransferase |
| YPL017C | [M] YPL017c strong similarity to LPD1P and other dihydrolipoamide dehydrogenases |
| YJL046W | [U] YJL046w similarity to E.coli lipoate-protein ligase A |
| Q-clique 30 | Function Annotation |
| YMR262W | [D] YMR262w similarity to S.pombe scn1 protein |
| YER061C | [E] CEM1 beta-keto-acyl-ACP synthase, mitochondrial |
| YPL148C | [F] PPT2 phosphopantetheine protein transferase |
| YHR208W | [G] BAT1 branched chain amino acid aminotransferase, mitochondrial |
| YJR148W | [G] BAT2 branched chain amino acid aminotransferase, cytosolic |
| YKL192C | [M] ACP1 mitochonrial acyl-carrier protein |
| YPL231W | [M] FAS2 fatty-acyl-CoA synthase, alpha chain |
| YOR221C | [M] MCT1 malonyl-CoA:ACP transferase |
| YJR057W | [M] CDC8 dTMP kinase |
| YKL182W | [M] FAS1 fatty-acyl-CoA synthase, beta chain |
| YDR454C | [M] GUK1 guanylate kinase |
| YMR024W | [P] MRPL3 ribosomal protein of the large subunit, mitochondrial |
| | |
| YCR003W | [P] MRPL32 ribosomal protein YmL32, mitochondrial |
| YMR239C | [T] RNT1 double-stranded ribonuclease |
| YMR239C YBL055C | [T] RNT1 double-stranded ribonuclease [U] YBL055c similarity to hypothetical S.pombe protein |
| YMR239C YBL055C Q-clique 33 | [T] RNT1 double-stranded ribonuclease [U] YBL055c similarity to hypothetical S.pombe protein Function Annotation |
| YMR239C YBL055C Q-clique 33 YCL017C | [T] RNT1 double-stranded ribonuclease [U] YBL055c similarity to hypothetical S.pombe protein Function Annotation [A] NFS1 regulates Iron-Sulfur cluster proteins, cellular Iron uptake, and Iron distribution |
| YMR239C YBL055C Q-clique 33 YCL017C YPR067W | [T] RNT1 double-stranded ribonuclease [U] YBL055c similarity to hypothetical S.pombe protein Function Annotation [A] NFS1 regulates Iron-Sulfur cluster proteins, cellular Iron uptake, andIron distribution [A] ISA2 mitochondrial protein required for iron metabolism |
| YMR239C YBL055C Q-clique 33 YCL017C YPR067W YLL027W | [T] RNT1 double-stranded ribonuclease [U] YBL055c similarity to hypothetical S.pombe protein Function Annotation [A] NFS1 regulates Iron-Sulfur cluster proteins, cellular Iron uptake, andIron distribution [A] ISA2 mitochondrial protein required for iron metabolism [A] ISA1 mitochondrial protein required for normal iron metabolism |
| YMR239C YBL055C Q-clique 33 YCL017C YPR067W YLL027W YGL018C | [T] RNT1 double-stranded ribonuclease [U] YBL055c similarity to hypothetical S.pombe protein Function Annotation [A] NFS1 regulates Iron-Sulfur cluster proteins, cellular Iron uptake, andIron distribution [A] ISA2 mitochondrial protein required for iron metabolism [A] ISA1 mitochondrial protein required for normal iron metabolism [F] JAC1 molecular chaperone |
| YMR239C YBL055C Q-clique 33 YCL017C YPR067W YLL027W YGL018C YPL135W | [T] RNT1 double-stranded ribonuclease [U] YBL055c similarity to hypothetical S.pombe protein Function Annotation [A] NFS1 regulates Iron-Sulfur cluster proteins, cellular Iron uptake, andIron distribution [A] ISA2 mitochondrial protein required for iron metabolism [A] ISA1 mitochondrial protein required for normal iron metabolism [F] JAC1 molecular chaperone [M] ISU1 strong similarity to nitrogen fixation protein (nifU) |
| YMR239C YBL055C Q-clique 33 YCL017C YPR067W YLL027W YGL018C YPL135W YOR226C | [T] RNT1 double-stranded ribonuclease [U] YBL055c similarity to hypothetical S.pombe protein Function Annotation [A] NFS1 regulates Iron-Sulfur cluster proteins, cellular Iron uptake, andIron distribution [A] ISA2 mitochondrial protein required for iron metabolism [A] ISA1 mitochondrial protein required for normal iron metabolism [F] JAC1 molecular chaperone [M] ISU1 strong similarity to nitrogen fixation protein (nifU) [M] ISU2 strong similarity to nitrogen fixation proteins |
| YMR239C YBL055C Q-clique 33 YCL017C YPR067W YLL027W YGL018C YPL135W YOR226C YLR231C | [T] RNT1 double-stranded ribonuclease [U] YBL055c similarity to hypothetical S.pombe protein Function Annotation [A] NFS1 regulates Iron-Sulfur cluster proteins, cellular Iron uptake, andIron distribution [A] ISA2 mitochondrial protein required for iron metabolism [A] ISA1 mitochondrial protein required for normal iron metabolism [F] JAC1 molecular chaperone [M] ISU1 strong similarity to nitrogen fixation protein (nifU) [M] ISU2 strong similarity to nitrogen fixation proteins [M] YLR231c strong similarity to rat kynureninase |
| YMR239C YBL055C Q-clique 33 YCL017C YPR067W YLL027W YGL018C YPL135W YOR226C YLR231C YKL067W | [T] RNT1 double-stranded ribonuclease [U] YBL055c similarity to hypothetical S.pombe protein Function Annotation [A] NFS1 regulates Iron-Sulfur cluster proteins, cellular Iron uptake, andIron distribution [A] ISA2 mitochondrial protein required for iron metabolism [A] ISA1 mitochondrial protein required for normal iron metabolism [F] JAC1 molecular chaperone [M] ISU1 strong similarity to nitrogen fixation protein (nifU) [M] ISU2 strong similarity to nitrogen fixation proteins [M] YLR231c strong similarity to rat kynureninase [M] YNK1 nucleoside diphosphate kinase |
| YMR239C YBL055C Q-clique 33 YCL017C YPR067W YLL027W YGL018C YPL135W YOR226C YLR231C YKL067W YDR283C | [T] RNT1 double-stranded ribonuclease [U] YBL055c similarity to hypothetical S.pombe protein Function Annotation [A] NFS1 regulates Iron-Sulfur cluster proteins, cellular Iron uptake, andIron distribution [A] ISA2 mitochondrial protein required for iron metabolism [A] ISA1 mitochondrial protein required for normal iron metabolism [F] JAC1 molecular chaperone [M] ISU1 strong similarity to nitrogen fixation protein (nifU) [M] ISU2 strong similarity to nitrogen fixation proteins [M] YLR231c strong similarity to rat kynureninase [M] YNK1 nucleoside diphosphate kinase [P] GCN2 ser/thr protein kinase |
| YMR239C YBL055C Q-clique 33 YCL017C YPR067W YLL027W YGL018C YPL135W YOR226C YLR231C YKL067W YDR283C YPR033C | [T] RNT1 double-stranded ribonuclease [U] YBL055c similarity to hypothetical S.pombe protein Function Annotation [A] NFS1 regulates Iron-Sulfur cluster proteins, cellular Iron uptake, andIron distribution [A] ISA2 mitochondrial protein required for iron metabolism [A] ISA1 mitochondrial protein required for normal iron metabolism [F] JAC1 molecular chaperone [M] ISU1 strong similarity to nitrogen fixation protein (nifU) [M] ISU2 strong similarity to nitrogen fixation proteins [M] YLR231c strong similarity to rat kynureninase [M] YNK1 nucleoside diphosphate kinase [P] GCN2 ser/thr protein kinase [P] HTS1 histidinetRNA ligase, mitochondrial |
| YMR239C YBL055C Q-clique 33 YCL017C YPR067W YLL027W YGL018C YPL135W YOR226C YLR231C YKL067W YDR283C YPR033C YPL252C | [T] RNT1 double-stranded ribonuclease [U] YBL055c similarity to hypothetical S.pombe protein Function Annotation [A] NFS1 regulates Iron-Sulfur cluster proteins, cellular Iron uptake, andIron distribution [A] ISA2 mitochondrial protein required for iron metabolism [A] ISA1 mitochondrial protein required for normal iron metabolism [F] JAC1 molecular chaperone [M] ISU1 strong similarity to nitrogen fixation protein (nifU) [M] ISU2 strong similarity to nitrogen fixation proteins [M] YLR231c strong similarity to rat kynureninase [M] YNK1 nucleoside diphosphate kinase [P] GCN2 ser/thr protein kinase [P] HTS1 histidinetRNA ligase, mitochondrial [U] YAH1 similarity to adrenodoxin and ferrodoxin |
| YMR239C YBL055C Q-clique 33 YCL017C YPR067W YLL027W YGL018C YPL135W YOR226C YLR231C YKL067W YDR283C YPR033C YPL252C Q-clique 34 | [T] RNT1 double-stranded ribonuclease [U] YBL055c similarity to hypothetical S.pombe protein Function Annotation [A] NFS1 regulates Iron-Sulfur cluster proteins, cellular Iron uptake, andIron distribution [A] ISA2 mitochondrial protein required for iron metabolism [A] ISA1 mitochondrial protein required for normal iron metabolism [F] JAC1 molecular chaperone [M] ISU1 strong similarity to nitrogen fixation protein (nifU) [M] ISU2 strong similarity to nitrogen fixation proteins [M] YLR231c strong similarity to rat kynureninase [M] YNK1 nucleoside diphosphate kinase [P] GCN2 ser/thr protein kinase [P] HTS1 histidinetRNA ligase, mitochondrial [U] YAH1 similarity to adrenodoxin and ferrodoxin Function Annotation |
| YMR239C YBL055C Q-clique 33 YCL017C YPR067W YLL027W YGL018C YPL135W YOR226C YLR231C YKL067W YDR283C YPR033C YPL252C Q-clique 34 YLL027W | [T] RNT1 double-stranded ribonuclease [U] YBL055c similarity to hypothetical S.pombe protein Function Annotation [A] NFS1 regulates Iron-Sulfur cluster proteins, cellular Iron uptake, andIron distribution [A] ISA2 mitochondrial protein required for iron metabolism [A] ISA1 mitochondrial protein required for normal iron metabolism [F] JAC1 molecular chaperone [M] ISU1 strong similarity to nitrogen fixation protein (nifU) [M] ISU2 strong similarity to nitrogen fixation proteins [M] YLR231c strong similarity to rat kynureninase [M] YNK1 nucleoside diphosphate kinase [P] GCN2 ser/thr protein kinase [P] HTS1 histidinetRNA ligase, mitochondrial [U] YAH1 similarity to adrenodoxin and ferrodoxin Function Annotation [A] ISA1 mitochondrial protein required for normal iron metabolism |
| YMR239C YBL055C Q-clique 33 YCL017C YPR067W YLL027W YGL018C YPL135W YOR226C YLR231C YKL067W YDR283C YPR033C YPL252C Q-clique 34 YLL027W YCL017C | [T] RNT1 double-stranded ribonuclease [U] YBL055c similarity to hypothetical S.pombe protein Function Annotation [A] NFS1 regulates Iron-Sulfur cluster proteins, cellular Iron uptake, andIron distribution [A] ISA2 mitochondrial protein required for iron metabolism [A] ISA1 mitochondrial protein required for normal iron metabolism [F] JAC1 molecular chaperone [M] ISU1 strong similarity to nitrogen fixation protein (nifU) [M] ISU2 strong similarity to nitrogen fixation proteins [M] YLR231c strong similarity to rat kynureninase [M] YNK1 nucleoside diphosphate kinase [P] GCN2 ser/thr protein kinase [P] HTS1 histidinetRNA ligase, mitochondrial [U] YAH1 similarity to adrenodoxin and ferrodoxin Function Annotation [A] ISA1 mitochondrial protein required for normal iron metabolism [A] NFS1 regulates Iron-Sulfur cluster proteins, cellular Iron uptake, andIron distribution |
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| YMR239C YBL055C Q-clique 33 YCL017C YPR067W YLL027W YGL018C YPL135W YOR226C YLR231C YKL067W YDR283C YPR033C YPL252C Q-clique 34 YLL027W YCL017C YPR067W YGL018C | [T] RNT1 double-stranded ribonuclease [U] YBL055c similarity to hypothetical S.pombe protein Function Annotation [A] NFS1 regulates Iron-Sulfur cluster proteins, cellular Iron uptake, andIron distribution [A] ISA2 mitochondrial protein required for iron metabolism [A] ISA1 mitochondrial protein required for normal iron metabolism [F] JAC1 molecular chaperone [M] ISU1 strong similarity to nitrogen fixation protein (nifU) [M] ISU2 strong similarity to nitrogen fixation proteins [M] YLR231c strong similarity to rat kynureninase [M] YNK1 nucleoside diphosphate kinase [P] GCN2 ser/thr protein kinase [P] HTS1 histidinetRNA ligase, mitochondrial [U] YAH1 similarity to adrenodoxin and ferrodoxin Function Annotation [A] ISA1 mitochondrial protein required for normal iron metabolism [A] NFS1 regulates Iron-Sulfur cluster proteins, cellular Iron uptake, andIron distribution [A] ISA2 mitochondrial protein required for iron metabolism [F] JAC1 molecular chaperone |
| YMR239C YBL055C Q-clique 33 YCL017C YPR067W YLL027W YGL018C YPL135W YOR226C YLR231C YKL067W YDR283C YPR033C YPL252C Q-clique 34 YLL027W YCL017C YPR067W YGL018C YLR231C | [T] RNT1 double-stranded ribonuclease [U] YBL055c similarity to hypothetical S.pombe protein Function Annotation [A] NFS1 regulates Iron-Sulfur cluster proteins, cellular Iron uptake, andIron distribution [A] ISA2 mitochondrial protein required for iron metabolism [A] ISA1 mitochondrial protein required for normal iron metabolism [F] JAC1 molecular chaperone [M] ISU1 strong similarity to nitrogen fixation protein (nifU) [M] ISU2 strong similarity to nitrogen fixation proteins [M] YLR231c strong similarity to rat kynureninase [M] YNK1 nucleoside diphosphate kinase [P] GCN2 ser/thr protein kinase [P] HTS1 histidinetRNA ligase, mitochondrial [U] YAH1 similarity to adrenodoxin and ferrodoxin Function Annotation [A] ISA1 mitochondrial protein required for normal iron metabolism [A] NFS1 regulates Iron-Sulfur cluster proteins, cellular Iron uptake, andIron distribution [A] ISA2 mitochondrial protein required for iron metabolism [F] JAC1 molecular chaperone [M] YLR231c strong similarity to rat kynureninase |
| YMR239C YBL055C Q-clique 33 YCL017C YPR067W YLL027W YGL018C YPL135W YOR226C YLR231C YKL067W YDR283C YPR033C YPL252C Q-clique 34 YLL027W YCL017C YPR067W YGL018C YLR231C YPL018C YLR231C | [T] RNT1 double-stranded ribonuclease [U] YBL055c similarity to hypothetical S.pombe protein Function Annotation [A] NFS1 regulates Iron-Sulfur cluster proteins, cellular Iron uptake, andIron distribution [A] ISA2 mitochondrial protein required for iron metabolism [A] ISA1 mitochondrial protein required for normal iron metabolism [F] JAC1 molecular chaperone [M] ISU1 strong similarity to nitrogen fixation protein (nifU) [M] ISU2 strong similarity to rat kynureninase [M] YLR231c strong similarity to rat kynureninase [M] YNK1 nucleoside diphosphate kinase [P] GCN2 ser/thr protein kinase [P] HTS1 histidinetRNA ligase, mitochondrial [U] YAH1 similarity to adrenodoxin and ferrodoxin Function Annotation [A] ISA1 mitochondrial protein required for normal iron metabolism [A] NFS1 regulates Iron-Sulfur cluster proteins, cellular Iron uptake, andIron distribution [A] ISA2 mitochondrial protein required for iron metabolism [F] JAC1 molecular chaperone [M] YLR231c strong similarity to rat kynureninase [M] ISU1 strong similarity to nitrogen fixation protein (nifU) |
| YMR239C YBL055C Q-clique 33 YCL017C YPR067W YLL027W YGL018C YPL135W YOR226C YLR231C YKL067W YDR283C YPR033C YPL252C Q-clique 34 YLL027W YCL017C YPR067W YGL018C YLR231C YLR231C YPL135W YKL040C | [T] RNT1 double-stranded ribonuclease [U] YBL055c similarity to hypothetical S.pombe protein Function Annotation [A] NFS1 regulates Iron-Sulfur cluster proteins, cellular Iron uptake, andIron distribution [A] ISA2 mitochondrial protein required for iron metabolism [A] ISA1 mitochondrial protein required for normal iron metabolism [F] JAC1 molecular chaperone [M] ISU1 strong similarity to nitrogen fixation protein (nifU) [M] ISU2 strong similarity to rat kynureninase [M] YLR231c strong similarity to rat kynureninase [M] YNK1 nucleoside diphosphate kinase [P] GCN2 ser/thr protein kinase [P] HTS1 histidinetRNA ligase, mitochondrial [U] YAH1 similarity to adrenodoxin and ferrodoxin Function Annotation [A] ISA1 mitochondrial protein required for normal iron metabolism [A] NFS1 regulates Iron-Sulfur cluster proteins, cellular Iron uptake, andIron distribution [A] ISA2 mitochondrial protein required for iron metabolism [F] JAC1 molecular chaperone [M] YLR231c strong similarity to rat kynureninase [M] ISU1 strong similarity to nitrogen fixation protein (nifU) [M] NFU1 iron homeostasis |
| YMR239C YBL055C Q-clique 33 YCL017C YPR067W YLL027W YGL018C YPL135W YOR226C YLR231C YKL067W YDR283C YPR033C YPL252C Q-clique 34 YLL027W YCL017C YPR067W YGL018C YLR231C YPR067W YGL018C YLR231C YPL135W YKL040C YOR226C | [T] RNT1 double-stranded ribonuclease [U] YBL055c similarity to hypothetical S.pombe protein Function Annotation [A] NFS1 regulates Iron-Sulfur cluster proteins, cellular Iron uptake, andIron distribution [A] ISA2 mitochondrial protein required for iron metabolism [A] ISA1 mitochondrial protein required for normal iron metabolism [F] JAC1 molecular chaperone [M] ISU1 strong similarity to nitrogen fixation protein (nifU) [M] ISU2 strong similarity to rat kynureninase [M] YLR231c strong similarity to rat kynureninase [M] YNK1 nucleoside diphosphate kinase [P] GCN2 ser/thr protein kinase [P] HTS1 histidinetRNA ligase, mitochondrial [U] YAH1 similarity to adrenodoxin and ferrodoxin Function Annotation [A] ISA1 mitochondrial protein required for normal iron metabolism [A] NFS1 regulates Iron-Sulfur cluster proteins, cellular Iron uptake, andIron distribution [A] ISA2 mitochondrial protein required for iron metabolism [F] JAC1 molecular chaperone [M] YLR231c strong similarity to rat kynureninase [M] ISU1 strong similarity to nitrogen fixation protein (nifU) [M] NFU1 iron homeostasis [M] ISU2 strong similarity to nitrogen fixation proteins |
| YMR239C YBL055C Q-clique 33 YCL017C YPR067W YLL027W YGL018C YPL135W YOR226C YLR231C YKL067W YDR283C YPR033C YPL252C Q-clique 34 YLL027W YCL017C YPR067W YGL018C YLR231C YPL135W YKL040C YOR226C YKL067W | [T] RNT1 double-stranded ribonuclease [U] YBL055c similarity to hypothetical S.pombe protein Function Annotation [A] NFS1 regulates Iron-Sulfur cluster proteins, cellular Iron uptake, andIron distribution [A] ISA2 mitochondrial protein required for iron metabolism [A] ISA1 mitochondrial protein required for normal iron metabolism [F] JAC1 molecular chaperone [M] ISU1 strong similarity to nitrogen fixation protein (nifU) [M] ISU2 strong similarity to nitrogen fixation proteins [M] YLR231c strong similarity to rat kynureninase [M] YNK1 nucleoside diphosphate kinase [P] GCN2 ser/thr protein kinase [P] HTS1 histidinetRNA ligase, mitochondrial [U] YAH1 similarity to adrenodoxin and ferrodoxin Function Annotation [A] ISA1 mitochondrial protein required for normal iron metabolism [A] NFS1 regulates Iron-Sulfur cluster proteins, cellular Iron uptake, andIron distribution [A] ISA2 mitochondrial protein required for iron metabolism [F] JAC1 molecular chaperone [M] YLR231c strong similarity to rat kynureninase [M] ISU1 strong similarity to nitrogen fixation protein (nifU) [M] NFU1 iron homeostasis [M] ISU2 strong similarity to nitrogen fixation proteins [M] YNK1 nucleoside diphosphate kinase |
| YMR239C YBL055C Q-clique 33 YCL017C YPR067W YLL027W YGL018C YPL135W YOR226C YLR231C YKL067W YDR283C YPR033C YPL252C Q-clique 34 YLL027W YCL017C YPR067W YGL018C YLR231C YLR231C YR067W YGL018C YLR231C YLR231C YPL135W YKL040C YOR226C YKL067W YPR033C | [T] RNT1 double-stranded ribonuclease [U] YBL055c similarity to hypothetical S.pombe protein Function Annotation [A] NFS1 regulates Iron-Sulfur cluster proteins, cellular Iron uptake, andIron distribution [A] ISA2 mitochondrial protein required for iron metabolism [A] ISA1 mitochondrial protein required for normal iron metabolism [F] JAC1 molecular chaperone [M] ISU1 strong similarity to nitrogen fixation protein (nifU) [M] ISU2 strong similarity to rat kynureninase [M] YLR231c strong similarity to rat kynureninase [M] YNK1 nucleoside diphosphate kinase [P] GCN2 ser/thr protein kinase [P] HTS1 histidinetRNA ligase, mitochondrial [U] YAH1 similarity to adrenodoxin and ferrodoxin Function Annotation [A] ISA1 mitochondrial protein required for normal iron metabolism [A] NFS1 regulates Iron-Sulfur cluster proteins, cellular Iron uptake, andIron distribution [A] ISA2 mitochondrial protein required for iron metabolism [F] JAC1 molecular chaperone [M] YLR231c strong similarity to rat kynureninase [M] ISU1 strong similarity to nitrogen fixation protein (nifU) [M] NFU1 iron homeostasis [M] ISU2 strong similarity to nitrogen fixation proteins [M] YNK1 nucleoside diphosphate kinase [P] HTS1 histidinetRNA ligase, mitochondrial |
| YMR239C YBL055C Q-clique 33 YCL017C YPR067W YLL027W YGL018C YPL135W YOR226C YLR231C YKL067W YDR283C YPR033C YPL252C Q-clique 34 YLL027W YCL017C YPR067W YGL018C YLR231C YPL135W YKL040C YOR226C YKL067W | [T] RNT1 double-stranded ribonuclease [U] YBL055c similarity to hypothetical S.pombe protein Function Annotation [A] NFS1 regulates Iron-Sulfur cluster proteins, cellular Iron uptake, andIron distribution [A] ISA2 mitochondrial protein required for iron metabolism [A] ISA1 mitochondrial protein required for normal iron metabolism [F] JAC1 molecular chaperone [M] ISU1 strong similarity to nitrogen fixation protein (nifU) [M] ISU2 strong similarity to nitrogen fixation proteins [M] YLR231c strong similarity to rat kynureninase [M] YNK1 nucleoside diphosphate kinase [P] GCN2 ser/thr protein kinase [P] HTS1 histidinetRNA ligase, mitochondrial [U] YAH1 similarity to adrenodoxin and ferrodoxin Function Annotation [A] ISA1 mitochondrial protein required for normal iron metabolism [A] NFS1 regulates Iron-Sulfur cluster proteins, cellular Iron uptake, andIron distribution [A] ISA2 mitochondrial protein required for iron metabolism [F] JAC1 molecular chaperone [M] YLR231c strong similarity to rat kynureninase [M] ISU1 strong similarity to nitrogen fixation protein (nifU) [M] NFU1 iron homeostasis [M] ISU2 strong similarity to nitrogen fixation proteins [M] YNK1 nucleoside diphosphate kinase |

| O aligna 25 | Function Annotation |
|--------------------|--|
| Q-clique 35 | Function Annotation [F] VMP.1189 strong similarity to synainets dehydrogeness |
| YMR118C | [E] YMR118c strong similarity to succinate dehydrogenase |
| YLL041C | [E] SDH2 succinate dehydrogenase iron-sulfur protein subunit |
| YDR148C | [E] KGD2 2-oxoglutarate dehydrogenase complex E2 component |
| YOR142W | [E] LSC1 succinate-CoA ligase alpha subunit |
| YER178W | [E] PDA1 pyruvate dehydrogenase (lipoamide) alpha chain precursor |
| YBR221C | [E] PDB1 pyruvate dehydrogenase (lipoamide) beta chain precursor |
| YIL125W | [E] KGD1 2-oxoglutarate dehydrogenase complex E1 component |
| YNL071W | [E] LAT1 dihydrolipoamide S-acetyltransferase |
| YGR244C | [E] LSC2 succinate-CoA ligase beta subunit |
| YKL141W | [E] SDH3 cytochrome b560 subunit of respiratory complex II |
| YGR193C | [E] PDX1 pyruvate dehydrogenase complex protein X |
| YOR375C | [G] GDH1 glutamate dehydrogenase (NADP+) |
| YFL018C | [G] LPD1 dihydrolipoamide dehydrogenase precursor |
| YAL062W | [G] GDH3 NADP-glutamate dehydrogenase |
| YML022W | [M] APT1 adenine phosphoribosyltransferase |
| YOR196C | [M] LIP5 lipoic acid synthase |
| YDR441C | [M] APT2 adenine phosphoribosyltransferase |
| YPL017C | [M] YPL017c strong similarity to LPD1P and other dihydrolipoamide dehydrogenases |
| YPL091W | [R] GLR1 glutathione reductase (NADPH) |
| YJL046W | [U] YJL046w similarity to E.coli lipoate-protein ligase A |
| Q-clique 36 | Function Annotation |
| YGL211W | [U] YGL211w similarity to M.jannaschii hypothetical proteins MJ1157 and MJ1478 |
| YNR016C | [M] ACC1 acetyl-CoA carboxylase |
| YNL026W | [U] YNL026w similarity to S.pombe hypothetical protein |
| YLR048W | [P] RPS0B 40S ribosomal protein p40 homolog B |
| YGR214W | [P] RPS0A 40S ribosomal protein p40 homolog A |
| YNL072W | [M] RNH35 RNase H(35), a 35 kDa ribonuclease H |
| YHR038W | [P] FIL1 Killed in Mutagen, sensitive to Diepoxybutane and/or Mitomycin C |
| YDL193W | [U] YDL193w similarity to N.crassa hypothetical 32 kDa protein |
| YMR101C | [M] SRT1 cis-prenyltransferase homologue |
| YBR029C | [M] CDS1 CDP-diacylglycerol synthase [F] RER2 cis-prenyltransferase, a key enzyme in dolichol synthesis |
| YBR002C | Function Annotation |
| Q-clique 37 | |
| YGL018C YOR226C | [F] JAC1 molecular chaperone [M] ISU2 strong similarity to nitrogen fixation proteins |
| YPR067W | [A] ISA2 mitochondrial protein required for iron metabolism |
| YPR033C | [P] HTS1 histidinetRNA ligase, mitochondrial |
| YPL252C | [U] YAH1 similarity to adrenodoxin and ferrodoxin |
| YLR231C | [M] YLR231c strong similarity to rat kynureninase |
| YPL135W | [M] ISU1 strong similarity to ritrogen fixation protein (nifU) |
| YCL017C | [A] NFS1 regulates Iron-Sulfur cluster proteins, cellular Iron uptake, and Iron distribution |
| YKL067W | [M] YNK1 nucleoside diphosphate kinase |
| YDR283C | [P] GCN2 ser/thr protein kinase |
| YLL027W | [A] ISA1 mitochondrial protein required for normal iron metabolism |
| Q-clique 38 | Function Annotation |
| YBR272C | [D] HSM3 mismatch repair protein |
| YOR261C | [F] RPN8 26S proteasome regulatory subunit |
| YER021W | [F] RPN3 26S proteasome regulatory subunit |
| YDR394W | [F] RPT3 26S proteasome regulatory subunit |
| YDL007W | [F] RPT2 26S proteasome regulatory subunit |
| YFR004W | [F] RPN11 26S proteasome regulatory subunit |
| YOR259C | [F] RPT4 26S proteasome regulatory subunit |
| YDL097C | [F] RPN6 subunit of the regulatory particle of the proteasome |
| YOR117W | [F] RPTS 26S proteasome regulatory subunit |
| TOKII/W | [1] Kt 15 205 proteasome regulatory subunit |

| VCI 049C | [E] DDT6 26C mastessame acquistem subvait |
|--------------------|--|
| YGL048C | [F] RPT6 26S proteasome regulatory subunit |
| YPR108W | [F] RPN7 subunit of the regulatory particle of the proteasome |
| YDL147W | [F] RPN5 subunit of the regulatory particle of the proteasome |
| YHR200W | [F] RPN10 26S proteasome regulatory subunit |
| YDR427W | [F] RPN9 subunit of the regulatory particle of the proteasome |
| YKL145W | [F] RPT1 26S proteasome regulatory subunit |
| YGR232W | [F] NAS6 possible homolog of human 26S proteasome regulatory subunit p28 |
| YJR109C | [G] CPA2 arginine-specific carbamoylphosphate synthase, large chain |
| YKL104C YLR421C | [M] GFA1 glucosaminefructose-6-phosphate transaminase [U] RPN13 weak similarity to human 42K membrane glycoprotein |
| | , , , |
| Q-clique 39 | Function Annotation |
| YGR135W | [F] PRE9 20S proteasome subunit Y13 (alpha3) |
| YER012W | [F] PRE1 20S proteasome subunit C11(beta4) |
| YMR314W | [F] PRE5 20S proteasome subunit(alpha6) |
| YOR362C YPR103W | [F] PRE10 20S proteasome subunit C1 (alpha7) |
| | [F] PRE2 20S proteasome subunit (beta5) |
| YER094C | [F] PUP3 20S proteasome subunit (beta3) |
| YGR253C | [F] PUP2 20S proteasome subunit(alpha5) |
| YOL038W | [F] PRE6 20S protessome subunit (alpha4) |
| YML092C | [F] PRE8 20S proteasome subunit Y7 (alpha2) |
| YBL041W | [F] PRE7 20S proteasome subunit(beta6) |
| YGL011C | [F] SCL1 20S proteasome subunit YC7ALPHA/Y8 (alpha1) |
| YFR050C | [F] PRE4 20S proteasome subunit(beta7) |
| YJL001W | [F] PRE3 20S proteasome subunit (beta1) |
| Q-clique 40 | Function Annotation |
| YBR002C | [F] RER2 cis-prenyltransferase, a key enzyme in dolichol synthesis |
| YBR029C | [M] CDS1 CDP-diacylglycerol synthase |
| YNL072W | [M] RNH35 RNase H(35), a 35 kDa ribonuclease H |
| YMR101C | [M] SRT1 cis-prenyltransferase homologue |
| YNR016C | [M] ACC1 acetyl-CoA carboxylase |
| YER087W YLR048W | [P] YER087w similarity to E.coli prolyl-tRNA synthetase [P] RPS0B 40S ribosomal protein p40 homolog B |
| YHR020W | [P] YHR020w strong similarity to human glutamyl-prolyl-tRNA synthetase and fruit fly |
| 1 HK020 W | multifunctional aminoacyl-tRNA synthetase |
| YHR038W | [P] FIL1 Killed in Mutagen, sensitive to Diepoxybutane and/or Mitomycin C |
| YHL004W | [P] MRP4 ribosomal protein of the small subunit, mitochondrial |
| YGR214W | [P] RPS0A 40S ribosomal protein p40 homolog A |
| YNL026W | [U] YNL026w similarity to S.pombe hypothetical protein |
| YDL193W | [U] YDL193w similarity to N.crassa hypothetical 32 kDa protein |
| YGL211W | [U] YGL211w similarity to M.jannaschii hypothetical proteins MJ1157 and MJ1478 |
| Q-clique 41 | Function Annotation |
| YJL046W | [U] YJL046w similarity to E.coli lipoate-protein ligase A |
| YMR118C | [E] YMR118c strong similarity to succinate dehydrogenase |
| YIL125W | [E] KGD1 2-oxoglutarate dehydrogenase complex E1 component |
| YOR142W | [E] LSC1 succinate-CoA ligase alpha subunit |
| YLL041C | [E] SDH2 succinate dehydrogenase iron-sulfur protein subunit |
| YGR244C | [E] LSC2 succinate CoA ligase beta subunit |
| YGR193C | [E] PDX1 pyruvate dehydrogenase complex protein X |
| YNL071W | [E] LAT1 dihydrolipoamide S-acetyltransferase |
| YER178W | [E] PDA1 pyruvate dehydrogenase (lipoamide) alpha chain precursor |
| YDR148C | [E] KGD2 2-oxoglutarate dehydrogenase complex E2 component |
| YOR196C | [M] LIP5 lipoic acid synthase |
| YFL018C | [G] LPD1 dihydrolipoamide dehydrogenase precursor |
| YKL141W | [E] SDH3 cytochrome b560 subunit of respiratory complex II |
| Q-clique 42 | Function Annotation |
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| VCDOOM | [D] MDDI 22 '1 |
|------------------------|--|
| YCR003W | [P] MRPL32 ribosomal protein YmL32, mitochondrial |
| YPL231W | [M] FAS2 fatty-acyl-CoA synthase, alpha chain |
| YKL182W | [M] FAS1 fatty-acyl-CoA synthase, beta chain |
| YJR057W | [M] CDC8 dTMP kinase |
| YMR262W | [D] YMR262w similarity to S.pombe scn1 protein |
| YOR221C | [M] MCT1 malonyl-CoA:ACP transferase |
| YJR148W | [G] BAT2 branched chain amino acid aminotransferase, cytosolic |
| YHR208W | [G] BAT1 branched chain amino acid aminotransferase, mitochondrial |
| YER061C | [E] CEM1 beta-keto-acyl-ACP synthase, mitochondrial |
| YDR454C | [M] GUK1 guanylate kinase |
| YKL192C | [M] ACP1 mitochonrial acyl-carrier protein |
| YBL055C | [U] YBL055c similarity to hypothetical S.pombe protein |
| Q-clique 43 | Function Annotation |
| YNL262W | [D] POL2 DNA-directed DNA polymerase epsilon, catalytic subunit A |
| YMR290C | [D] HAS1 helicase associated with SET1P |
| YAL035W | [P] FUN12 general translation factor eIF2 homolog |
| YGR162W | [P] TIF4631 mRNA cap-binding protein (eIF4F), 150K subunit |
| YOL139C | [P] CDC33 translation initiation factor eIF4E |
| YGL049C | [P] TIF4632 mRNA cap-binding protein (eIF4F), 130K subunit |
| YDL051W | [T] LHP1 RNA binding protein |
| YLR175W | [T] CBF5 putative rRNA pseuduridine synthase |
| YOR310C | [T] NOP58 required for pre-18S rRNA processing |
| YPL043W | [T] NOP4 nucleolar protein |
| YLR197W | [T] SIK1 involved in pre-rRNA processing |
| YGL120C | [T] PRP43 involved in spliceosome disassembly |
| YOL041C | [U] NOP12 weak similarity to M.sativa NUM1, hnRNP protein from C. tentans and D. |
| | melanogaster, murine/bovine poly(A) binding protein II, and NSR1P |
| YBL004W | [U] YBL004w weak similarity to Papaya ringspot virus polyprotein |
| YDL213C | [U] FYV14 weak similarity to potato small nuclear ribonucleoprotein U2B and human |
| VCD 145W | splicing factor homolog |
| YGR145W | [U] YGR145w similarity to C.elegans hypothetical protein |
| YDR496C YKL014C | [U] PUF6 similarity to hypothetical human and C.elegans proteins |
| YPL012W | [U] YKL014c similarity to hypothetical protein SPCC14G10.02 S. pombe [U] RRP12 hypothetical protein |
| | Function Annotation |
| Q-clique 44 YDR292C | [F] SRP101 signal recognition particle receptor, alpha chain |
| YML094W | [F] GIM5 Gim complex component |
| YJL189W | [P] RPL39 60S large subunit ribosomal protein L39.e |
| YLR406C | [P] RPL31B 60S large subunit ribosomal protein L31.e.c12 |
| YMR242C | [P] RPL20A 60s large subunit ribosomal protein |
| YOL121C | [P] RPS19A 40S small subunit ribosomal protein S19.e |
| YNL302C | [P] RPS19B 40S small subunit ribosomal protein S19.e |
| YDL075W | [P] RPL31A 60S large subunit ribosomal protein L31.e |
| YOR312C | [P] RPL20B 60S large subunit ribosomal protein |
| YPR016C | [P] TIF6 translation initiation factor 6 (eIF6) |
| YMR074C | [U] YMR074c strong similarity to hypothetical S. pombe protein |
| Q-clique 45 | Function Annotation |
| YGR240C | [E] PFK1 6-phosphofructokinase, alpha subunit |
| YJR109C | [G] CPA2 arginine-specific carbamoylphosphate synthase, large chain |
| YDR007W | [G] TRP1 phosphoribosylanthranilate isomerase |
| YDR127W | [G] ARO1 arom pentafunctional enzyme |
| YER090W | [G] TRP2 anthranilate synthase component I |
| YKL211C | [G] TRP3 anthranilate synthase component II |
| YNR033W | [M] ABZ1 para-aminobenzoate synthase |
| YKL104C | [M] GFA1 glucosaminefructose-6-phosphate transaminase |
| | r 2 C comment to the first contraction of the contr |

| YMR012W | [P] CLU1 translation initiation factor eIF3 (p135 subunit) |
|-------------|---|
| YGL245W | [P] YGL245w strong similarity to glutaminetRNA ligase |
| Q-clique 46 | Function Annotation |
| YML094W | [F] GIM5 Gim complex component |
| YDR292C | [F] SRP101 signal recognition particle receptor, alpha chain |
| YMR242C | [P] RPL20A 60s large subunit ribosomal protein |
| YOL121C | [P] RPS19A 40S small subunit ribosomal protein S19.e |
| YOR312C | [P] RPL20B 60S large subunit ribosomal protein |
| YDL075W | [P] RPL31A 60S large subunit ribosomal protein L31.e |
| YPR016C | [P] TIF6 translation initiation factor 6 (eIF6) |
| YNL302C | [P] RPS19B 40S small subunit ribosomal protein S19.e |
| YJL189W | [P] RPL39 60S large subunit ribosomal protein L39.e |
| YLR406C | [P] RPL31B 60S large subunit ribosomal protein L31.e.c12 |
| YMR074C | [U] YMR074c strong similarity to hypothetical S. pombe protein |
| Q-clique 47 | Function Annotation |
| YMR089C | [F] YTA12 protease of the SEC18/CDC48/PAS1 family of ATPases (AAA) |
| YER017C | [F] AFG3 protease of the SEC18/CDC48/PAS1 family of ATPases (AAA) |
| YPR024W | [F] YME1 protease of the SEC18/CDC48/PAS1 family of ATPases (AAA) |
| YER090W | [G] TRP2 anthranilate synthase component I |
| YDR007W | [G] TRP1 phosphoribosylanthranilate isomerase |
| YGL026C | [G] TRP5 tryptophan synthase |
| YKL211C | [G] TRP3 anthranilate synthase component II |
| YNR033W | [M] ABZ1 para-aminobenzoate synthase |
| YOR241W | [M] MET7 tetrahydrofolylpolyglutamate synthase |
| YMR113W | [M] FOL3 dihydrofolate synthetase |
| YMR278W | [M] YMR278w similarity to phosphomannomutases |
| YNL256W | [M] FOL1 Dihydroneopterin aldolase, dihydro-6-hydroxymethylpterin pyrophosphokinase, |
| | dihydropteroate synthetase |
| YGR267C | [M] FOL2 GTP cyclohydrolase I |
| YEL058W | [M] PCM1 phosphoacetylglucosamine mutase |
| YKL132C | [M] RMA1 similarity to B.subtilis folC protein and strong similarity to YMR113w |
| Q-clique 48 | Function Annotation |
| YBR002C | [F] RER2 cis-prenyltransferase, a key enzyme in dolichol synthesis |
| YDL142C | [M] CRD1 cardiolipin synthase |
| YBR042C | [M] CST26 weak similarity to 1-acyl-sn-glycerol-3-phosphate acyltransferase from Brassica |
| | napus |
| YMR101C | [M] SRT1 cis-prenyltransferase homologue |
| YPR113W | [M] PIS1 CDP diacylglycerolinositol 3-phosphatidyltransferase |
| YNR016C | [M] ACC1 acetyl-CoA carboxylase |
| YNL072W | [M] RNH35 RNase H(35), a 35 kDa ribonuclease H |
| YBR029C | [M] CDS1 CDP-diacylglycerol synthase |
| YDL052C | [M] SLC1 fatty acyltransferase |
| YLR048W | [P] RPS0B 40S ribosomal protein p40 homolog B |
| YHR038W | [P] FIL1 Killed in Mutagen, sensitive to Diepoxybutane and/or Mitomycin C |
| YGR214W | [P] RPS0A 40S ribosomal protein p40 homolog A |
| YNL026W | [U] YNL026w similarity to S.pombe hypothetical protein |
| YDL193W | [U] YDL193w similarity to N.crassa hypothetical 32 kDa protein |
| YDR018C | [U] YDR018c strong similarity to hypothetical protein YBR042c |

Note: All quasi-cliques and their members along with function annotation (48 quasi-cliques and 511 proteins in total) are listed above. Q-clique N: the No. of quasi-cliques.